

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:32:54 ; Search time 24.9231 Seconds
(without alignments)
104.146 Million cell updates/sec

Title: US-09-673-490B-5

Perfect score: 158

Sequence: 1 CKSKGAKCSKLMYDCSGSGCTVGRC 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PTR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	72.2	25	2 JH0700	omega-conotoxin MV
2	107.5	68.0	29	2 JH0699	omega-conotoxin MV
3	96.5	61.1	26	2 C44379	omega-conotoxin SV
4	96	60.8	29	2 A58537	omega-conotoxin MV
5	93	58.9	25	2 JH0701	omega-conotoxin MV
6	71.5	45.3	52	2 T10299	conotoxin-like pro
7	70.5	44.6	73	1 NTKN6G	omega-conotoxin GV
8	68.5	43.4	29	2 B43620	omega-conotoxin GV
9	64.5	40.8	29	2 A43620	omega-conotoxin GV
10	62.5	39.6	37	2 E44007	aptootoxin III - tr
11	59.5	37.7	60	1 SMH01A	metallothionein 1A
12	59.5	37.7	66	2 S58086	metallothionein 3
13	59.5	37.7	68	2 A46034	metallothionein 3,
14	59.5	37.7	68	2 I67866	growth inhibitory
15	58.5	37.0	325	2 H71271	hypothetical prote
16	58	36.7	27	2 S19619	delta-conotoxin Tx
17	58	36.7	78	2 S12513	delta-conotoxin Tx
18	57	36.1	61	2 S47652	metallothionein 1X
19	57	36.1	318	2 T05569	hypothetical prote
20	56.5	35.8	63	2 S08191	metallothionein 2
21	56.5	35.8	68	2 B46034	metallothionein 3,
22	56.5	35.8	68	2 S44392	metallothionein 3,
23	56.5	35.8	68	2 JC6521	metallothionein II
24	56	35.4	72	2 S39418	metallothionein 10
25	56	35.4	558	2 JC5204	60K cysteine-rich
26	55.5	35.1	2150	2 T32497	hypothetical prote
27	55	34.8	60	2 JC2420	metallothionein
28	55	34.8	61	2 S54333	metallothionein-2E
29	55	34.8	686	2 T25987	hypothetical prote

30	54.5	34.5	53	2 T30499	conotoxin-like pro
31	54.5	34.5	53	2 T10405	conotoxin-like pro
32	54.5	34.5	63	2 S08190	metallothionein 1
33	54	34.2	27	2 S55030	CAP5 protein - ant
34	54	34.2	556	1 S12602	60K cysteine-rich
35	54	34.2	556	2 A86560	60 kDa Cysteine-ri
36	53.5	33.9	61	1 SMH01A	metallothionein 1A
37	53.5	33.9	72	2 S39419	metallothionein 10
38	53.5	33.9	170	2 T09601	DNAJ protein homol
39	53.5	33.9	249	2 T32060	hypothetical prote
40	53.5	33.9	423	2 T09338	DNAJ-like protein
41	53.5	33.9	689	2 T52060	protein MEDEA lim
42	53	33.5	61	2 S00811	metallothionein II
43	53	33.5	61	2 B23889	metallothionein 2
44	53	33.5	358	2 T23802	hypothetical prote
45	52.5	33.2	43	2 S18174	metallothionein -

ALIGNMENTS

RESULT 1

JH0700

omega-conotoxin MVIIA [validated] - cone shell (Conus magus) ;

C:Species: Conus magus (magus cone)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Sep-2000

C:Accession: JH0700; C60133; A34115

R:Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J
Neuron 9, 69-77, 1992

A:Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.

A:Reference number: JH0699; MUID:92337922; PMID:1352986

A:Accession: JH0700

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-25 <HIL>

R:Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de S-

Science 230, 1338-1343, 1985

A:Title: Peptide neurotoxins from fish-hunting cone snails.

A:Reference number: A43620; MUID:86070213; PMID:4071055

A:Accession: C60133

A:Molecule type: protein

A:Residues: 1-25 <OLI>

R:Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.

Biochemistry 26, 2086-2090, 1987

A:Title: Neuronal calcium channel antagonists. Discrimination between calcium channel

A:Reference number: A34115; MUID:87299637; PMID:2441741

A:Contents: annotation

R:Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.

submitted to the Brookhaven Protein Data Bank, August 1996

A:Reference number: A67648; PDB:IMV1

A:Contents: annotation; conformation by (1)H-NMR, residues 1-25

R:Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.

J. Mol. Biol. 263, 297-310, 1996

A:Title: A consensus structure for omega-conotoxins with different selectivities for

A:Reference number: A58619; MUID:97073382; PMID:8913308

A:Contents: annotation; conformation by (1)H-NMR

R:Kohn, T.; Kim, J.I.; Kobayashi, K.; Koder, Y.; Maeda, T.; Sato, K.

submitted to the Brookhaven Protein Data Bank, April 1995

A:Reference number: A66296; PDB:10MG

A:Contents: annotation; conformation by (1)H-NMR, residues 1-25

R:Kohn, T.; Kim, J.I.; Kobayashi, K.; Koder, Y.; Maeda, T.; Sato, K.

Biochemistry 34, 10256-10265, 1995

A:Title: Three-dimensional structure in solution of the calcium channel blocker omega

A:Reference number: A58622; MUID:95367555; PMID:7640281

A:Contents: annotation; conformation by (1)H-NMR

C:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel

F:1-16, 8-20, 15-25/disulfide bonds: #status predicted

F:25/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 72.2%; Score 114; DB 2; Length 25;

Best Local Similarity 70.4%; Pred. No. 8e-07;

Matches 19; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

A: Experimental source: venom
A: Note: sequence extracted from NCBI backbone (NCBIP:116002): structure confirmed by chR.Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
Submitted to the Brookhaven Protein Data Bank, August 1996
A: Reference number: PDB:1MVJ
A: Contents: annotation; conformation
K.Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.

JH0701
omega-conotoxin MVIIIB - cone shell (Conus magus)
C:Species: Conus magus (magus cone)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change*23-May-1997
C:Accession: JH0701; B34115
R:Hillaryard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.
Neuron 9, 69-77, 1992
A:Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.
A:Reference number: JH0699; MUID:92337922; PMID:1352986
A:Accession: JH0701
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-25 <H1L>
R:Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, G.
Biochemistry 26, 2086-2090, 1987
A:Title: Neuronal calcium channel antagonists. Discrimination between calcium channels.
A:Reference number: A34115; MUID:87299637; PMID:2441741

A:Accession: B34115
A:Molecule type: protein
A:Residues: 1-25 <OLI>
C:Superfamily: omega-conotoxin
C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel
F:1-16, 8-20, 15-25/Disulfide bonds: #status predicted
F:25/Modified site: amidated carboxyl end (Cys) #status predicted

Query Match 58.9%; Score 93; DB 2; Length 25;
 Best Local Similarity 55.6%; Pred. No. 0.0002; 1;
 Matches 15; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 1 CKSKGAKCKLMYDCCSGSGGTGRC 27
 ||||| : |||||: |||
 Db 1 CKKGASCHRTSYDCCTGSCNR--GKC 25

RESULT 6

T10299
 conotoxin-like protein 2 - Orgyia pseudotsugata nuclear polyhedrosis virus
 C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpNPV
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
 C:Accession: T10299
 R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
 Virology 229, 381-399, 1997
 A:Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
 A:Reference number: Z17011; MUID:97271300; PMID:9126251
 A:Accession: T10299
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-52 <AHR>
 A:Cross-references: EMBL:U75930; NID:g2934903; PID:g19111276

Query Match 45.3%; Score 71.5; DB 2; Length 52;
 Best Local Similarity 44.4%; Pred. No. 0.095;
 Matches 12; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 1 CKSKGAKCKLMYDCCSGSGGTGRC 27
 | | | : | : | | | : | |
 Db 24 CTETGRNC-QYSYECCSGACSAAGFC 49

RESULT 7

NTKN6G
 omega-conotoxin GVIB precursor [validated] - cone shell (Conus geographus)
 N:Alternate names: shaker peptide GVIB
 N:Contains: omega-conotoxin GVIA; omega-conotoxin GVIC
 C:Species: Conus geographus (geography cone)
 C:Date: 25-Feb-1985 #sequence_revision 23-Mar-1995 #text_change 15-Sep-2000
 C:Accession: A44006; A60133; B60133; A01785
 R:Colledge, C.J.; Hunsperger, J.P.; Imperial, J.S.; Hillyard, D.R.
 Toxicon 30, 1111-1116, 1992
 A:Title: Precursor structure of omega-conotoxin GVIA determined from a cDNA clone.
 A:Reference number: A44006; MUID:93069286; PMID:1440648
 A:Accession: A44006
 A:Molecule type: mRNA
 A:Residues: 1-73 <COL>
 A:Cross-references: GB:M84612; NID:g156520; PIDN:AAA81590.1; PID:g1070393
 A:Experimental source: venom duct
 A:Note: sequence extracted from NCBI backbone (NCBIN:119531, NCBIP:119532)
 R:Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santis
 Science 230, 1338-1343, 1985
 A:Title: Peptide neurotoxins from fish-hunting cone snails.
 A:Reference number: A43620; MUID:86070213; PMID:4071055
 A:Accession: A60133
 A:Molecule type: protein
 A:Residues: 46-73 <OLI>
 A:Accession: B60133
 A:Molecule type: protein
 A:Residues: 46-71 <OL2>
 R:Olivera, B.M.; McIntosh, J.M.; Cruz, L.J.; Luque, F.A.; Gray, W.R.
 Biochemistry 23, 5087-5090, 1984
 A:Title: Purification and sequence of a presynaptic peptide toxin from Conus geographus
 A:Reference number: A01785; MUID:85072972; PMID:6509012
 A:Accession: A01785
 A:Molecule type: protein
 A:Residues: 46-72 <OL3>
 R:Nishikuchi, Y.; Kumagaya, K.; Noda, Y.; Watanabe, T.X.; Sakakibara, S.
 Biopolymers 25, S61-S68, 1986
 A:Title: Synthesis and secondary-structure determination of omega-conotoxin GVIA: a 27-p

A:Reference number: A49017; MUID:87049928; PMID:3779030

A:Contents: annotation
 A:Note: disulfide bonds determined and confirmed by chemical synthesis
 R:Davis, J.H.; Bradley, E.K.; Miljanich, G.P.; Nadasdi, L.; Ramachandran, J.; Basus,
 submitted to the Brookhaven Protein Data Bank, April 1993
 A:Reference number: A51894; PDB:1OMC
 A:Contents: annotation; conformation by (1)H-NMR, residues 46-72
 R:Davis, J.H.; Bradley, E.K.; Miljanich, G.P.; Nadasdi, L.; Ramachandran, J.; Basus,
 Biochemistry 32, 7396-7405, 1993
 A:Title: Solution structure of omega-conotoxin GVIA using 2-D NMR spectroscopy and r-
 A:Reference number: A58536; MUID:93332945; PMID:8338837
 A:Contents: annotation; conformation by (1)H-NMR
 R:Pallaghy, P.K.; Duggan, B.M.; Pennington, M.W.; Norton, R.S.;
 submitted to the Brookhaven Protein Data Bank, August 1993
 A:Reference number: A51089; PDB:1CCO
 A:Contents: annotation; conformation by (1)H-NMR, residues 46-72
 C:Comment: There are several types of conotoxins: alpha, acting on postsynaptic membr
 neurotoxin.

C:Superfamily: omega-conotoxin
 C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-45/Domain: propeptide #status predicted <PRO>
 F:46-73/Product: omega-conotoxin GVIB #status experimental <MAT1>
 F:46-72/Product: omega-conotoxin GVIA #status experimental <MAT2>
 F:46-71/Product: omega-conotoxin GVIC #status experimental <MAT3>
 F:46-61,53-64,60-71/Disulfide bonds: #status experimental
 F:49,55,66/Modified site: 4-hydroxyproline (Pro) #status experimental
 F:72/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

Query Match 44.6%; Score 70.5; DB 1; Length 73;
 Best Local Similarity 48.1%; Pred. No. 0.15;
 Matches 13; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 CKSKGAKCKLMYDCCSGSGGTGRC 27
 ||| | : || | : || |
 Db 46 CKSPGSCSPTSYNCCR-SCNPYTKRC 71

RESULT 8

B43620
 omega-conotoxin GVIB - cone shell (Conus geographus)
 N:Alternate names: shaker peptide GVIB
 C:Species: Conus geographus (geography cone)
 C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 23-May-1997
 C:Accession: B43620
 R:Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de S
 Science 230, 1338-1343, 1985
 A:Title: Peptide neurotoxins from fish-hunting cone snails.
 A:Reference number: A43620; MUID:86070213; PMID:4071055
 A:Accession: B43620
 A:Molecule type: protein
 A:Residues: 1-29 <OLI>
 C:Superfamily: omega-conotoxin
 C:Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproli
 F:16,18-19,15-26/Disulfide bonds: #status predicted
 F:4,7/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 43.4%; Score 68.5; DB 2; Length 29;
 Best Local Similarity 48.1%; Pred. No. 0.14;
 Matches 13; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 CKSKGAKCKLMYDCCSGSGGTGRC 27
 ||| | : || | : || |
 Db 1 CKSPGTPCSGRMRDCT-SCLSYSNKC 26

RESULT 9

A43620
 omega-conotoxin GVIIA - cone shell (Conus geographus)
 N:Alternate names: shaker peptide GVIIA
 C:Species: Conus geographus (geography cone)
 C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 23-May-1997
 C:Accession: A43620

I67866
growth inhibitory factor - mouse
C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 20-Aug-1999
C:Accession: I67866
R:Naruse, S.; Igarashi, S.; Furuya, T.; Kobayashi, H.; Miyatake, T.; Tsuji, S.
Gene 144, 283-287, 1994
A:Title: Structures of the human and mouse growth inhibitory factor-encoding genes.
A:Reference number: I53803; MUID:94314230; PMID:8039715
A:Accession: I67866
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-68 <RES>
A:Cross-references: GB:S72046; NID:g565191; PIDN:AAB31397.1; PID:g565192
C:Genetics:
A:Gene: GIF
A:Introns: 11/1; 33/1
C:Superfamily: metallothionein

Query Match 37.7%; Score 59.5; DB 2; Length 68;
Best Local Similarity 40.7%; Pred. No. 2.7;
Matches 11; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

QY 1 CKSKGAKSKLMYDCSGSGCTVGRG 27
|| || ||: ||| | : |
Db 20 CKCKGCKCTNCKKSCCS-CCPAGEKRC 45

RESULT 15
H71271
hypothetical protein TP0856 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: H71271
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwirson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McGdell, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: H71271
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-325 <COL>
A:Cross-references: GB:AE001256; GB:AE000520; NID:g3323171; PIDN:AAC65828.1; PID:g332317
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0856

Query Match 37.0%; Score 58.5; DB 2; Length 325;
Best Local Similarity 44.4%; Pred. No. 9.6;
Matches 12; Conservative 4; Mismatches 6; Indels 5; Gaps 2;

QY 1 CKSKGAKSKLMYDCSGSGCTVGRG 27
|::|:| | ||| |::| |
Db 230 CRATGEQCK----TCSGRCTG-VGTC 251

Search completed: February 26, 2003, 08:40:27
Job time : 25.9231 secs

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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:39:54 ; Search time 17.3077 Seconds
(without alignments)
58.846 Million cell updates/sec

Title: US-09-673-490B-5

Perfect score: 158

Sequence: 1 CKSKGAKCKLMYDCSGSGCTVGRC 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174566 seqs, 37721826 residues

Total number of hits satisfying chosen parameters: 174566

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	63.5	40.2	29	9 US-09-749-637A-208	Sequence 208, App
2	63	39.9	1076	9 US-10-028-072-219	Sequence 219, App
3	63	39.9	1076	9 US-10-121-049-219	Sequence 219, App
4	63	39.9	1076	9 US-10-123-904-219	Sequence 219, App
5	63	39.9	1076	9 US-10-140-470-219	Sequence 219, App
6	63	39.9	1076	9 US-10-175-746-219	Sequence 219, App
7	63	39.9	1076	9 US-10-176-918-219	Sequence 219, App
8	63	39.9	1076	9 US-10-176-921-219	Sequence 219, App
9	63	39.9	1076	9 US-10-137-865-219	Sequence 219, App
10	63	39.9	1076	9 US-10-140-474-219	Sequence 219, App
11	63	39.9	1076	9 US-10-142-431-219	Sequence 219, App
12	63	39.9	1076	9 US-10-143-114-219	Sequence 219, App
13	61	38.6	27	9 US-09-749-637A-27	Sequence 27, Appl
14	61	38.6	27	9 US-09-749-637A-28	Sequence 28, Appl
15	61	38.6	27	9 US-09-749-637A-31	Sequence 31, Appl
16	61	38.6	27	9 US-09-749-637A-34	Sequence 34, Appl
17	60	38.0	26	9 US-09-749-637A-43	Sequence 43, Appl
18	60	38.0	27	9 US-09-749-637A-23	Sequence 23, Appl
19	60	38.0	27	9 US-09-749-637A-24	Sequence 24, Appl

20	60	38.0	76	9 US-09-749-637A-207	Sequence 207, App
21	59	37.3	77	9 US-09-749-637A-42	Sequence 42, Appl
22	58	36.7	78	9 US-09-749-637A-22	Sequence 22, Appl
23	58	36.7	78	9 US-09-749-637A-26	Sequence 26, Appl
24	58	36.7	78	9 US-09-749-637A-30	Sequence 30, Appl
25	58	36.7	78	9 US-09-749-637A-33	Sequence 33, Appl
26	57.5	36.4	31	10 US-09-894-882-458	Sequence 458, App
27	57.5	36.4	44	10 US-09-894-882-496	Sequence 496, App
28	57.5	36.4	70	10 US-09-894-882-238	Sequence 238, App
29	57	36.1	3907	9 US-10-029-217A-24	Sequence 24, Appl
30	56.5	35.8	2211	9 US-10-096-961-1	Sequence 1, Appl
31	56.5	35.8	4679	10 US-09-804-898-2	Sequence 2, Appl
32	56	35.4	25	9 US-09-749-637A-307	Sequence 307, Appl
33	56	35.4	32	9 US-09-749-637A-108	Sequence 108, App
34	56	35.4	76	9 US-09-749-637A-306	Sequence 306, App
35	56	35.4	179	10 US-09-764-853-635	Sequence 635, App
36	56	35.4	179	10 US-09-764-898-205	Sequence 205, App
37	56	35.4	384	9 US-09-924-400-326	Sequence 326, App
38	56	35.4	384	9 US-09-924-400-332	Sequence 332, App
39	56	35.4	384	10 US-09-810-936-332	Sequence 332, App
40	56	35.4	384	10 US-09-810-936-332	Sequence 332, App
41	56	35.4	1200	10 US-09-826-508-3	Sequence 3, Appl
42	55.5	35.1	3046	9 US-09-759-1308-441	Sequence 441, App
43	55	34.8	80	9 US-09-749-637A-65	Sequence 65, Appl
44	55	34.8	80	9 US-09-749-637A-86	Sequence 86, Appl
45	55	34.8	1400	10 US-09-879-957-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-749-637A-208
; Sequence 208, Application US/09749637A
; Patent No. US20020173449A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 208
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Conus distans
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(29)
; OTHER INFORMATION: xaa at residues 3, 6 and 17 may be Glu or gamma-carboxy-Glu;
; OTHER INFORMATION: at residue 12 may be Pro or hydroxy-Pro
US-09-749-637A-208

Query Match 40.2%; Score 63.5; DB 9; Length 29;
Best Local Similarity 44.4%; Pred. No. 0.54;
Matches 12; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

Oy 1 CKSGAKCSKLMYDCSGSCSTVGRC 27
| : : | | | | : | | | |
Db 1 CNXAQXCTQ-NXDCCSXSNCFVGR 26

RESULT 2

US-10-028-072-219
; Sequence 219, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028.072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
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; PRIOR APPLICATION NUMBER: 60/062816
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; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063561
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; PRIOR FILING DATE: 1997-10-29
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; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR FILING DATE: 1997-11-24
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069212
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069278
; PRIOR FILING DATE: 1997-12-11
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; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069694
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 60/072320
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: 60/079728
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081695
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081818
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28


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; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086414
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; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

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Query Match 39.9%; Score 63; DB 9; Length 1076;
 Best Local Similarity 43.5%; Pred. No. 11;
 Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

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QY 5 GAKCSKLMYDCCSGSGTGVRC 27
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Db 142 GACATTGTCCCAAGCTGTGAC 164

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RESULT 3

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US-10-121-049-219
; Sequence 219, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-219

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Query Match 39.9%; Score 63; DB 9; Length 1076;
 Best Local Similarity 43.5%; Pred. No. 11;
 Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

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QY 5 GAKCSKLMYDCCSGSGTGVRC 27
    |||  |||  |||  |||  |||  |||
Db 142 GACATTGTCCCAAGCTGTGAC 164

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RESULT 4
US-10-123-904-219
; Sequence 219, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219

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; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-219

Query Match          39.9%; Score 63; DB 9; Length 1076;
Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 5 GAKCSKLMYDCSGSCSGCTVGRG 27
   |||: ||: ||| |||
Db 142 GAACATTGTCCTCCAAAGCTGTGAC 164

RESULT 5
US-10-140-470-219
; Sequence 219, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-219
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Query Match          39.9%; Score 63; DB 9; Length 1076;
Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 5 GAKCSKLMYDCSGSCSGCTVGRG 27
   |||: ||: ||| |||
Db 142 GAACATTGTCCTCCAAAGCTGTGAC 164
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RESULT 6
US-10-175-746-219
; Sequence 219, Application US/10175746
; Publication No. US200300227270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
```

```
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-219
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Query Match          39.9%; Score 63; DB 9; Length 1076;
Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 5 GAKCSKLMYDCSGSCSGCTVGRG 27
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Db 142 GAACATTGTCCTCCAAAGCTGTGAC 164
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RESULT 7
US-10-176-918-219
; Sequence 219, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-219
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Query Match          39.9%; Score 63; DB 9; Length 1076;
Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 5 GAKCSKLMYDCSGSCSGCTVGRG 27
   |||: ||: ||| |||
Db 142 GAACATTGTCCTCCAAAGCTGTGAC 164
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RESULT 8

US-10-176-921-219
; Sequence 219, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC288
; CURRENT APPLICATION NUMBER: US/10/176, 921
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-921-219

Query Match 39.9%; Score 63; DB 9; Length 1076;

Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 5 GAKCSKLMYDCCSGSCSGTVGRC 27
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DB 142 GAACATTGTCCCAAGCTGTGAC 164

RESULT 9

US-10-137-865-219
; Sequence 219, Application US/10137865
; Publication No. US20030032155A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC154
; CURRENT APPLICATION NUMBER: US/10/137, 865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550

Query Match 39.9%; Score 63; DB 9; Length 1076;

Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 5 GAKCSKLMYDCCSGSCSGTVGRC 27
|| | : || : || : || : ||
DB 142 GAACATTGTCCCAAGCTGTGAC 164

; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-865-219

Query Match 39.9%; Score 63; DB 9; Length 1076;
Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 5 GAKCSKLMYDCCSGSCSGTVGRC 27
|| | : || : || : || : ||
DB 142 GAACATTGTCCCAAGCTGTGAC 164

RESULT 10

US-10-140-474-219
; Sequence 219, Application US/10140474
; Publication No. US20030032156A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC162
; CURRENT APPLICATION NUMBER: US/10/140, 474
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-474-219

Query Match 39.9%; Score 63; DB 9; Length 1076;
Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 5 GAKCSKLMYDCCSGSCSGTVGRC 27
|| | : || : || : || : ||
DB 142 GAACATTGTCCCAAGCTGTGAC 164

RESULT 11

US-10-142-431-219
; Sequence 219, Application US/10142431
; Publication No. US20030036179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

Query Match 39.9%; Score 63; DB 9; Length 1076;

Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 5 GAKCSKLMYDCCSGSCSGTVGRC 27
|| | : || : || : || : ||
DB 142 GAACATTGTCCCAAGCTGTGAC 164

; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-431-219

Query Match 39.9%; Score 63; DB 9; Length 1076;
Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 5 GAKSKLMYDCSCSGSCSTVGRC 27
|||: ||: |::|::|
Db 142 GAACATTGTCACAGCTTGAC 164

RESULT 12
US-10-143-114-219
; Sequence 219, Application US/10143114
; Publication No. US20030036180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C211
; CURRENT APPLICATION NUMBER: US/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-143-114-219

Query Match 39.9%; Score 63; DB 9; Length 1076;
Best Local Similarity 43.5%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 5 GAKSKLMYDCSCSGSCSTVGRC 27
|||: ||: |::|::|
Db 142 GAACATTGTCACAGCTTGAC 164

RESULT 13
US-09-749-637A-27
; Sequence 27, Application US/09749637A
; Patent No. US20020173449A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus magus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may
; OTHER INFORMATION: Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-1-
; OTHER INFORMATION: r, mono-Iodo-Tyr, di-Iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
US-09-749-637A-27

Query Match 38.6%; Score 61; DB 9; Length 27;
Best Local Similarity 45.0%; Pred. No. 0.94;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 CKSKGAKCSKLMYDCSCGSC 20
|||: |::|::|
Db 2 CKQSGXMCNLLDQNCDCGXC 21

RESULT 14
US-09-749-637A-28
; Sequence 28, Application US/09749637A
; Patent No. US20020173449A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263

Search completed: February 26, 2003, 08:53:01
Job time : 19.3077 secs

;; PRIOR FILING DATE: 2000-06-26
;; PRIOR APPLICATION NUMBER: US 60/173,754
;; PRIOR FILING DATE: 1999-12-30
;; NUMBER OF SEQ ID NOS: 409
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 28
;; LENGTH: 27
;; TYPE: PRT
;; ORGANISM: Conus textile
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (1)..(27)
;; OTHER INFORMATION: Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
;; OTHER INFORMATION: Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
;; OTHER INFORMATION: r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
US-09-749-637A-28

Query Match 38.6%; Score 61; DB 9; Length 27;
Best Local Similarity 45.0%; Pred. No. 0.94;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 CKSKGAKCKLMYDCCSGC 20
DB 2 CKSGXMCNLLDQNCDCGXC 21

RESULT 15
US-09-749-637A-31
;; Sequence 31, Application US/09749637A
;; Patent No. US20020173449A1
;; GENERAL INFORMATION:
;; APPLICANT: University of Utah Research Foundation
;; APPLICANT: Cognetix, Inc.
;; APPLICANT: Olivera, Baldomero M.
;; APPLICANT: Cartier, G. Edward
;; APPLICANT: Watkins, Maren
;; APPLICANT: Hillyard, David R.
;; APPLICANT: McIntosh, J. Michael
;; APPLICANT: Layer, Richard T.
;; APPLICANT: Jones, Robert M.
;; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
;; FILE REFERENCE: 2314-227
;; CURRENT APPLICATION NUMBER: US/09/749,637A
;; CURRENT FILING DATE: 2000-12-28
;; PRIOR APPLICATION NUMBER: US 60/243,412
;; PRIOR FILING DATE: 2000-10-27
;; PRIOR APPLICATION NUMBER: US60/219,440
;; PRIOR FILING DATE: 2000-07-20
;; PRIOR APPLICATION NUMBER: US 60/214,263
;; PRIOR FILING DATE: 2000-06-26
;; PRIOR APPLICATION NUMBER: US 60/173,754
;; PRIOR FILING DATE: 1999-12-30
;; NUMBER OF SEQ ID NOS: 409
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 31
;; LENGTH: 27
;; TYPE: PRT
;; ORGANISM: Conus distans
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (1)..(27)
;; OTHER INFORMATION: Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
;; OTHER INFORMATION: Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
;; OTHER INFORMATION: r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
US-09-749-637A-31

Query Match 38.6%; Score 61; DB 9; Length 27;
Best Local Similarity 45.0%; Pred. No. 0.94;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 CKSKGAKCKLMYDCCSGC 20
DB 2 CKSGXMCNLLDQNCDCGXC 21

ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-198
US-07-789-913-16

Query Match 73.4%; Score 116; DB 1; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.2e-06;
Matches 19; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 CKSGAKCSKLMYDCSCSGTGVRC 27
||| |||||:|||||:||||: 1:1
Db 1 CKGKAKCSRLMYDCTGSCAS--GKC 25

RESULT 2
US-08-049-794-16
; Sequence 16, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 19930415
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-198, FIGURE 2
; US-08-049-794-16

Query Match 73.4%; Score 116; DB 1; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.2e-06;
Matches 19; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 CKSGAKCSKLMYDCSCSGTGVRC 27
||| |||||:|||||:||||: 1:1
Db 1 CKGKAKCSRLMYDCTGSCAS--GKC 25

RESULT 3
US-08-496-847-16
; Sequence 16, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristibati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496.847
; FILING DATE: 27-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-198, FIGURE 2
; US-08-496-847-16

Query Match 73.4%; Score 116; DB 1; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.2e-06;
Matches 19; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 CKSGAKCSKLMYDCSCSGTGVRC 27
||| |||||:|||||:||||: 1:1
Db 1 CKGKAKCSRLMYDCTGSCAS--GKC 25

RESULT 4
US-08-742-774-16
; Sequence 16, Application US/08742774
; Patent No. 5824645
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 1993-APR-15
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-198, FIGURE 2
US-08-742-774-16

Query Match 73.4%; Score 116; DB 2; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.2e-06;
Matches 19; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
QY 1 CKSGAKCSKLMYDCGSGCGTGVRC 27
|| |||||:||||:||||: 1:1
DB 1 CKGKGAKCSRLMYDCTGTGSCAS--GKC 25
RESULT 5
US-08-675-354-16
Sequence 16, Application US/08675354
Patent No. 5859186
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C.
APPLICANT: VALENTINO, KAREN L.
APPLICANT: MTJANICH, GEORGE P.
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354

FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-198, FIGURE 2
US-08-675-354-16
Query Match 73.4%; Score 116; DB 2; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.2e-06;
Matches 19; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
QY 1 CKSGAKCSKLMYDCGSGCGTGVRC 27
|| |||||:||||:||||: 1:1
DB 1 CKGKGAKCSRLMYDCTGTGSCAS--GKC 25

RESULT 6
US-08-965-918-16
Sequence 16, Application US/08965918
Patent No. 5891849
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-198, FIGURE 2
US-08-965-918-16

Query Match 73.4%; Score 116; DB 2; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.2e-06;
Matches 19; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 CKSGAKCSKLMYDCSCSGCTVGRC 27
|| |||||:|||||:|:|
Db 1 CKGKGAKCSRLMYDCCTGSCAS--GKC 25

RESULT 7
US-09-138-439-16
; Sequence 16, Application US/09138439
; Patent No. 5994305
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/138.439
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049.794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-198, FIGURE 2
US-09-138-439-16

Query Match 73.4%; Score 116; DB 2; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.2e-06;
Matches 19; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
```

```
Qy 1 CKSGAKCSKLMYDCSCSGCTVGRC 27
|| |||||:|||||:|:|
Db 1 CKGKGAKCSRLMYDCCTGSCAS--GKC 25

RESULT 8
US-08-613-400A-16
; Sequence 16, Application US/08613400A
; Patent No. 6054429
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gadbois, Theresa
; APPLICANT: Pettus, Mark, R.
; APPLICANT: Luther, Robert, R.
; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613.400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-198, FIGURE 2
US-08-613-400A-16

Query Match 73.4%; Score 116; DB 3; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.2e-06;
Matches 19; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 CKSGAKCSKLMYDCSCSGCTVGRC-27
|| |||||:|||||:|:|
Db 1 CKGKGAKCSRLMYDCCTGSCAS--GKC 25

RESULT 9
US-09-298-017-16
; Sequence 16, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
```

```

; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-198, FIGURE 2
US-09-298-017-16

Query Match 73.4%; Score 116; DB 3; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.2e-06;
Matches 19; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 CKSGKAKCSKLMYDCGSGSGTGVRG 27
Db 1 CKGKGAKCSRLMYDCTGTGSCAS--GKC 25

RESULT 10
US-09-392-979A-16
; Sequence 16, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-198, FIGURE 2
US-09-392-979A-16

Query Match 73.4%; Score 116; DB 4; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.2e-06;
Matches 19; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 CKSGKAKCSKLMYDCGSGSGTGVRG 27
Db 1 CKGKGAKCSRLMYDCTGTGSCAS--GKC 25

RESULT 11
US-07-789-913-1
; Sequence 1, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,913
; FILING DATE: 19911112
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; FILING DATE: 22-NOV-1989

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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
; US-08-049-794-1

Query Match 72.2%; Score 114; DB 1; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.9e-06;
Matches 19; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 CKGKAGCSKLMYDCCSGSGTGVGR 27
   |||||||:|||||:||||| 1:
Db 1 CKGKAGCSRLMYDCCGTGSCRS--GKC 25

RESULT 13
US-08-496-847-1
; Sequence 1, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,847
; FILING DATE: 27-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
; US-08-496-847-1

Query Match 72.2%; Score 114; DB 1; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.9e-06;
Matches 19; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 CKGKAGCSKLMYDCCSGSGTGVGR 27
   |||||||:|||||:||||| 1:
Db 1 CKGKAGCSRLMYDCCGTGSCRS--GKC 25

RESULT 14
US-08-742-774-1
; Sequence 1, Application US/08742774

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Patent No. 5824645
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE: 03-JUL-1996
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
US-08-742-774-1
Query Match 72.2%; Score 114; DB 2; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.9e-06;
Matches 19; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
QY 1 CRKSGAKSKLMYDCGSGSGTVGRC 27
|| |||||:|||||:| 1:1
Db 1 CRKGGAKCSRLMYDCTGSCRS--GKC 25
RESULT 15
US-08-675-354-1
Sequence 1, Application US/08675354
Patent No. 5859186
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
US-08-675-354-1
Query Match 72.2%; Score 114; DB 2; Length 25;
Best Local Similarity 70.4%; Pred. No. 1.9e-06;
Matches 19; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
QY 1 CRKSGAKSKLMYDCGSGSGTVGRC 27
|| |||||:|||||:| 1:1
Db 1 CRKGGAKCSRLMYDCTGSCRS--GKC 25
Search completed: February 26, 2003, 08:41:04
Job time : 23.5385 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run On: February 26, 2003, 08:30:59 ; Search time 60.9231 seconds
(without alignments)
59.054 Million cell updates/sec

Title: US-09-673-490B-5
Perfect score: 158
Sequence: 1 CKSRGAKCSKLMYDCSGSGTGVGR 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_101002:*

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- 2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
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- 9: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
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- 12: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
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- 15: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
- 16: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
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- 18: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	158	100.0	27	21 AAY43711	Amino acid sequenc
2	158	100.0	27	21 AAY43728	Amino acid sequenc
3	158	100.0	28	21 AAY43727	Amino acid sequenc
4	158	100.0	28	21 AAY43729	Amino acid sequenc
5	158	100.0	28	21 AAY43730	Amino acid sequenc
6	158	100.0	73	21 AAY43730	Amino acid sequenc
7	155	98.1	27	21 AAY43717	Amino acid sequenc
8	155	98.1	27	21 AAY43718	Amino acid sequenc
9	155	98.1	27	21 AAY43719	Amino acid sequenc
10	155	98.1	27	21 AAY43725	Amino acid sequenc

11	154	97.5	27	21 AAY43720	Amino acid sequenc
12	154	97.5	27	21 AAY43722	Amino acid sequenc
13	153	96.8	27	21 AAY43721	Amino acid sequenc
14	152	96.2	27	21 AAY43724	Amino acid sequenc
15	152	96.2	27	21 AAY43726	Amino acid sequenc
16	152	96.2	27	21 AAY43731	Amino acid sequenc
17	152	96.2	27	21 AAY43734	Amino acid sequenc
18	152	96.2	27	21 AAY43735	Amino acid sequenc
19	152	96.2	27	21 AAY43736	Amino acid sequenc
20	151	95.6	27	21 AAY43713	Amino acid sequenc
21	149	94.3	27	21 AAY43723	Amino acid sequenc
22	149	94.3	27	21 AAY43732	Amino acid sequenc
23	144	91.1	27	23 ABB96890	Omega-conopeptide
24	144	91.1	73	23 ABB96675	Omega-conopeptide
25	143	90.5	27	21 AAY43733	Amino acid sequenc
26	138	87.3	27	23 ABB96781	Omega-conopeptide
27	134	84.8	27	23 ABB96842	Omega-conopeptide
28	134	84.8	73	23 ABB96626	Omega-conopeptide
29	128	81.0	27	23 ABB96729	Omega-conopeptide
30	122	77.2	27	23 ABB96835	Omega-conopeptide
31	122	77.2	73	23 ABB96631	Omega-conopeptide
32	116	73.4	25	14 AAR37770	SNX-198. Syntheti
33	116	73.4	25	14 AAR36625	SNX-198. Syntheti
34	116	73.4	25	18 AAW19562	SNX-198. omega con
35	116	73.4	25	18 AAW12982	Omega conopeptide
36	116	73.4	25	19 AAW72622	Conus genus analog
37	116	73.4	25	20 AAW95581	Analog omega-conop
38	116	73.4	25	21 AAB14367	Omega-conopeptide
39	116	73.4	25	21 AAY58490	Analog omega con
40	116	73.4	25	22 AAB19459	Sequence of an ome
41	114	72.2	25	14 AAR32777	MVIIA omega conoto
42	114	72.2	25	14 AAR37752	MVIIA/SNX-111. Sy
43	114	72.2	25	14 AAR39608	MVIIA/SNX111. Syn
44	114	72.2	25	16 AAR76089	Omega conotoxin MV
45	114	72.2	25	18 AAW19569	SNX-279, omega con

ALIGNMENTS

RESULT 1
AAY43711
ID AAY43711 standard; peptide; 27 AA.
XX AAY43711;
AC
XX
XX
DF 11-FEB-2000 (first entry)
XX
DE Amino acid sequence of an omega-conotoxin CVID.

Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
neuronal damage reduction; ischemia; analgesia; opiate analgesia;
schizophrenia; stimulant induced psychosis; hypertension; inflammation;
bronchotension; neuropathic pain; voltage sensitive calcium channel.

OS Conus catus.
XX
XX WO9954350-A1.
XX
XX 28-OCT-1999.
XX
XX 16-APR-1999; 99WO-AU00288.
PR 16-APR-1998; 98AU-0002989.
PR 01-FEB-1999; 99AU-0008419.
XX
XX (UYQU) UNIV QUEENSLAND.
PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX
XX WPI; 2000-013226/01.

Novel peptides used for the treatment of disorders and diseases where

PT blockage of the N-type calcium channels is required -

PS Claim 6; Page 45; 81pp; English.

XX The present sequence represents an omega-conotoxin. Omega-conotoxins
CC are isolated from venoms of predatory marine snails, and have a
CC selectivity for N-type calcium channels over P/Q type channels, and so
CC block N-type calcium channels. The omega-conotoxins of the invention
CC can be used in any disease or disorder where blockage of N-type calcium
CC channels is required, e.g. in the reduction of neuronal damage following
CC ischemia, production of analgesia, or enhancement of opiate analgesia,
CC in the treatment of schizophrenia, stimulant induced psychoses,
CC hypertension, inflammation, and diseases which cause bronchotension,
CC and also in the inhibition of progression of neuropathic pain. They can
CC also be used in a screen to identify compounds with activity at N-type
CC voltage sensitive calcium channels.

XX Sequence 27 AA;

Query Match 100.0%; Score 158; DB 21; Length 27;

Best Local Similarity 100.0%; Pred. No. 6.1e-11;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKSKGAKCSKLMYDCCSGSCSGTGVGRG 27

DB 1 CKSKGAKCSKLMYDCCSGSCSGTGVGRG 27

RESULT 2

RAY43728
ID AAY43728 standard; peptide; 27 AA.

AC AAY43728;

DT 11-FEB-2000 (first entry)

DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

OS Synthetic.

OS Conus catus.

XX Key Location/Qualifiers

FT Misc-difference 27 /note= "free carboxyl at the C-terminal"

PN WO9954350-A1.

XX 28-OCT-1999.

PF 16-APR-1999; 99WO-AU00288.

XX 16-APR-1998; 98AU-0002989.

PR 01-FEB-1999; 99AU-0008419.

XX (UYQU) UNIV QUEENSLAND.

PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX WPI; 2000-013226/01.

PT Novel peptides used for the treatment of disorders and diseases where
PT blockage of the N-type calcium channels is required -

PS Claim 6; Page 45; 81pp; English.

XX AAY43718-36 represent derivatives of omega-conotoxin CVID.

CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
CC have a selectivity for N-type calcium channels over P/Q type channels.

CC and so block N-type calcium channels. The omega-conotoxins of the
CC invention can be used in any disease or disorder where blockage of N-type
CC calcium channels is required, e.g. in the reduction of neuronal damage
CC following ischemia, production of analgesia, or enhancement of opiate
CC analgesia, in the treatment of schizophrenia, stimulant induced
CC psychoses, hypertension, inflammation, and diseases which cause
CC bronchotension, and also in the inhibition of progression of neuropathic
CC pain. They can also be used in a screen to identify compounds with
CC activity at N-type voltage sensitive calcium channels.

XX Sequence 27 AA;

Query Match 100.0%; Score 158; DB 21; Length 27;

Best Local Similarity 100.0%; Pred. No. 6.1e-11;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKSKGAKCSKLMYDCCSGSCSGTGVGRG 27

DB 1 CKSKGAKCSKLMYDCCSGSCSGTGVGRG 27

RESULT 3

AAY43727

ID AAY43727 standard; peptide; 28 AA.

AC AAY43727;

DT 11-FEB-2000 (first entry)

DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

OS Synthetic.

OS Conus catus.

PN WO9954350-A1.

PD 28-OCT-1999.

XX 16-APR-1999; 99WO-AU00288.

XX 16-APR-1998; 98AU-0002989.

PR 01-FEB-1999; 99AU-0008419.

XX (UYQU) UNIV QUEENSLAND.

PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX WPI; 2000-013226/01.

PT Novel peptides used for the treatment of disorders and diseases where
PT blockage of the N-type calcium channels is required -

PS Claim 6; Page 45; 81pp; English.

XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
CC have a selectivity for N-type calcium channels over P/Q type channels,
CC and so block N-type calcium channels. The omega-conotoxins of the
CC invention can be used in any disease or disorder where blockage of N-type
CC calcium channels is required, e.g. in the reduction of neuronal damage
CC following ischemia, production of analgesia, or enhancement of opiate
CC analgesia, in the treatment of schizophrenia, stimulant induced
CC psychoses, hypertension, inflammation, and diseases which cause
CC bronchotension, and also in the inhibition of progression of neuropathic
CC pain. They can also be used in a screen to identify compounds with
CC activity at N-type voltage sensitive calcium channels.

XX Sequence 28 AA;

Query Match 100.0%; Score 158; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.3e-11;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKSKGAKCSKLMYDCCSGSGTGVRC 27
 |||||
 DB 1 CKSKGAKCSKLMYDCCSGSGTGVRC 27

RESULT 4

AA43729
 ID AAY43729 standard; peptide; 28 AA.

AC AAY43729;
 XX
 DT 11-FEB-2000 (first entry)
 XX

DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX Synthetic.

OS Conus catus.

XX WO9954350-A1.

PN 28-OCT-1999.

XX 16-APR-1999; 99WO-AU00288.

XX 16-APR-1998; 98AU-0002989.

PR 01-FEB-1999; 99AU-0008419.

XX (UYQU) UNIV QUEENSLAND.

PA Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

PI WPI; 2000-013226/01.

XX Novel peptides used for the treatment of disorders and diseases where
 blockage of the N-type calcium channels is required -

PS Claim 6; Page 46; 81pp; English.

XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.

XX Sequence 28 AA;

Query Match 100.0%; Score 158; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.3e-11;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKSKGAKCSKLMYDCCSGSGTGVRC 27
 |||||
 DB 2 CKSKGAKCSKLMYDCCSGSGTGVRC 28

RESULT 5

AA43730

ID AAY43730 standard; peptide; 28 AA.

XX AC AAY43730;

XX DT 11-FEB-2000 (first entry)

DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX Synthetic.

OS Conus catus.

XX Key Location/Qualifiers

FH Modified-site 1 /note= "acetylated residue"

FT WO9954350-A1.

PN 28-OCT-1999.

XX 16-APR-1999; 99WO-AU00288.

XX 16-APR-1998; 98AU-0002989.

PR 01-FEB-1999; 99AU-0008419.

XX (UYQU) UNIV QUEENSLAND.

XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

PI WPI; 2000-013226/01.

XX Novel peptides used for the treatment of disorders and diseases where
 blockage of the N-type calcium channels is required -

PS Claim 6; Page 46; 81pp; English.

XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.

XX Sequence 28 AA;

Query Match 100.0%; Score 158; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.3e-11;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKSKGAKCSKLMYDCCSGSGTGVRC 27
 |||||
 DB 2 CKSKGAKCSKLMYDCCSGSGTGVRC 28

RESULT 6

AA43717

ID AAY43717 standard; peptide; 73 AA.

XX AC AAY43717;

XX DT 11-FEB-2000 (first entry)

XX

DE Amino acid sequence of an omega-conotoxin CVID.
 KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX
 OS Conus catus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..45
 FT /note= "signal peptide"
 FT Protein 46..73
 FT /note= "mature protein"
 XX
 XX WO9954350-A1.
 PN
 XX 28-OCT-1999.
 PD
 XX
 XX 16-APR-1999; 99WO-AU00288.
 PF
 XX 16-APR-1998; 98AU-0002989.
 PR
 PR 01-FEB-1999; 99AU-0008419.
 XX
 XX (UYQU) UNIV QUEENSLAND.
 PA
 XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 PI WPI; 2000-013226/01.
 XX
 DR N-PSDB; AAZ30311.
 DR
 XX Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -
 PT
 XX Disclosure; Page 60-61; 81pp; English.
 PS
 XX The present sequence represents an omega-conotoxin. Omega-conotoxins
 CC are isolated from venoms of predatory marine snails, and have a
 CC selectivity for N-type calcium channels over P/Q type channels, and so
 CC block N-type calcium channels. The omega-conotoxins of the invention
 CC can be used in any disease or disorder where blockage of N-type calcium
 CC channels is required, e.g. in the reduction of neuronal damage following
 CC ischemia, production of analgesia, or enhancement of opiate analgesia,
 CC in the treatment of schizophrenia, stimulant induced psychoses,
 CC hypertension, inflammation, and diseases which cause bronchotension,
 CC and also in the inhibition of progression of neuropathic pain. They can
 CC also be used in a screen to identify compounds with activity at N-type
 CC voltage sensitive calcium channels;
 XX
 SQ Sequence 73 AA;

Query Match 100.0%; Score 158; DB 21; Length 73;
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CKSGAKCSKLMYDCSCSGSGTVGRC 27
 |||||
 DB 46 CKSGAKCSKLMYDCSCSGSGTVGRC 72

RESULT 7
 AAY43712
 ID AAY43712 standard; peptide; 27 AA.
 XX
 AC AAY43712;
 XX
 DT 11-FEB-2000 (first entry)
 XX
 DE Amino acid sequence of an omega-conotoxin R10-CVID.
 XX
 KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;

KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX
 OS Synthetic.
 OS Conus catus.
 XX
 PN WO9954350-A1.
 XX
 PD 28-OCT-1999.
 XX
 XX 16-APR-1999; 99WO-AU00288.
 PF
 PR 16-APR-1998; 98AU-0002989.
 PR
 PR 01-FEB-1999; 99AU-0008419.
 XX
 XX (UYQU) UNIV QUEENSLAND.
 PA
 XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 PI WPI; 2000-013226/01.
 XX
 DR Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -
 PT
 XX Claim 6; Page 45; 81pp; English.
 PS
 XX The present sequence represents a modified version of omega-conotoxin
 CC CVID (see AAY43712). Omega-conotoxins are isolated from venoms of
 CC predatory marine snails, and have a selectivity for N-type calcium
 CC channels over P/Q type channels, and so block N-type calcium channels.
 CC The omega-conotoxins of the invention can be used in any disease or
 CC disorder where blockage of N-type calcium channels is required, e.g. in
 CC the reduction of neuronal damage following ischemia, production of
 CC analgesia, or enhancement of opiate analgesia, in the treatment of
 CC schizophrenia, stimulant induced psychoses, hypertension, inflammation,
 CC and diseases which cause bronchotension, and also in the inhibition of
 CC progression of neuropathic pain. They can also be used in a screen to
 CC identify compounds with activity at N-type voltage sensitive calcium
 CC channels.
 XX
 SQ Sequence 27 AA;

Query Match 98.1%; Score 155; DB 21; Length 27;
 Best Local Similarity 96.3%; Pred. No. 1.3e-10;
 Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CKSGAKCSKLMYDCSCSGSGTVGRC 27
 |||||
 DB 1 CKSGAKCSRLMYDCCSGSGSGTVGRC 27

RESULT 8
 AAY43718
 ID AAY43718 standard; peptide; 27 AA.
 XX
 AC AAY43718;
 XX
 DT 11-FEB-2000 (first entry)
 XX
 DE Amino acid sequence of an omega-conotoxin derivative of CVID.
 XX
 KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX
 OS Synthetic.
 OS Conus catus.
 XX
 PN WO9954350-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 16-APR-1999; 99WO-AU00288.

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XX 16-APR-1998; 98AU-0002989.
PR 01-FEB-1999; 99AU-0008419.
PA (UYQU ) UNIV QUEENSLAND.
XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX WPI; 2000-013226/01.
XX Novel peptides used for the treatment of disorders and diseases where
PT blockage of the N-type calcium channels is required -
XX Claim 6; Page 45; 8lpp; English.
XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
CC have a selectivity for N-type calcium channels over P/Q type channels,
CC and so block N-type calcium channels. The omega-conotoxins of the
CC calcium channels is required, e.g. in the reduction of neuronal damage
CC following ischemia, production of analgesia, or enhancement of opiate
CC analgesia, in the treatment of schizophrenia, stimulant induced
CC psychoses, hypertension, inflammation, and diseases which cause
CC bronchotension, and also in the inhibition of progression of neuropathic
CC pain. They can also be used in a screen to identify compounds with
CC activity at N-type voltage sensitive calcium channels.
XX SQ Sequence 27 AA;
XX Query Match 98.1%; Score 155; DB 21; Length 27;
XX Best Local Similarity 96.3%; Pred. No. 1.3e-10;
XX Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRSKGAKCSKLMYDCSGSCSGTVGRC 27
DB 1 CRSKGAKCSKLMYDCSGSCSGTVGRC 27
|:|||||:|||||:|||||:|||||:|||||:
RESULT 9
AAY43719
ID AAY43719 standard; peptide; 27 AA.
XX AAY43719;
XX 11-FEB-2000 (first entry)
XX Amino acid sequence of an omega-conotoxin derivative of CVID.
XX Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
XX Synthetic.
OS Conus catus.
XX WO9954350-A1.
XX 28-OCT-1999.
XX 16-APR-1999; 99WO-AU00288.
XX 16-APR-1998; 98AU-0002989.
PR 01-FEB-1999; 99AU-0008419.
XX (UYQU ) UNIV QUEENSLAND.
XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX WPI; 2000-013226/01.
XX Novel peptides used for the treatment of disorders and diseases where
PT blockage of the N-type calcium channels is required -
XX Claim 6; Page 45; 8lpp; English.
XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
CC have a selectivity for N-type calcium channels over P/Q type channels,
CC and so block N-type calcium channels. The omega-conotoxins of the
CC calcium channels is required, e.g. in the reduction of neuronal damage
CC following ischemia, production of analgesia, or enhancement of opiate
CC analgesia, in the treatment of schizophrenia, stimulant induced
CC psychoses, hypertension, inflammation, and diseases which cause
CC bronchotension, and also in the inhibition of progression of neuropathic
CC pain. They can also be used in a screen to identify compounds with
CC activity at N-type voltage sensitive calcium channels.
XX SQ Sequence 27 AA;
XX Query Match 98.1%; Score 155; DB 21; Length 27;
XX Best Local Similarity 96.3%; Pred. No. 1.3e-10;
XX Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRSKGAKCSKLMYDCSGSCSGTVGRC 27
DB 1 CRSKGAKCSKLMYDCSGSCSGTVGRC 27
|:|||||:|||||:|||||:|||||:|||||:
RESULT 10
AAY43725
ID AAY43725 standard; peptide; 27 AA.
XX AAY43725;
XX 11-FEB-2000 (first entry)
XX Amino acid sequence of an omega-conotoxin derivative of CVID.
XX Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
XX Synthetic.
OS Conus catus.
XX WO9954350-A1.
XX 28-OCT-1999.
XX 16-APR-1999; 99WO-AU00288.
XX 16-APR-1998; 98AU-0002989.
PR 01-FEB-1999; 99AU-0008419.
XX (UYQU ) UNIV QUEENSLAND.
XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX WPI; 2000-013226/01.
XX Novel peptides used for the treatment of disorders and diseases where
PT blockage of the N-type calcium channels is required -
XX Claim 6; Page 45; 8lpp; English.
XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
CC have a selectivity for N-type calcium channels over P/Q type channels,
CC and so block N-type calcium channels. The omega-conotoxins of the
CC calcium channels is required, e.g. in the reduction of neuronal damage
CC following ischemia, production of analgesia, or enhancement of opiate
CC analgesia, in the treatment of schizophrenia, stimulant induced
CC psychoses, hypertension, inflammation, and diseases which cause
CC bronchotension, and also in the inhibition of progression of neuropathic
CC pain. They can also be used in a screen to identify compounds with
CC activity at N-type voltage sensitive calcium channels.
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Query Match 97.5%; Score 154; DB 21; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.7e-10;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

AA43721	
ID	AA43721 standard; peptide; 27 AA.
XX	
AC	AA43721;

XX 11-FEB-2000 (first entry)
 XX Amino acid sequence of an omega-conotoxin derivative of CVID.
 DE Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 XX neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX Synthetic.
 OS Conus catus.
 XX WO9954350-A1.
 XX 28-OCT-1999.
 XX 16-APR-1999; 99WO-AU00288.
 XX 16-APR-1998; 98AU-0002989.
 PR 01-FEB-1999; 99AU-0008419.
 XX (UYQU) UNIV QUEENSLAND.
 XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX WPI; 2000-013226/01.
 XX Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -
 XX Claim 6; Page 45; 81pp; English.
 XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, and diseases which cause
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.
 XX Sequence 27 AA;
 SQ Query Match 96.8%; Score 153; DB 21; Length 27;
 Best Local Similarity 96.3%; Pred. NO. 2.2e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CKSKGAKCSKLMYDCSCSGCTGVGRC 27
 DB 1 CKSKGAKCSKLMYDCSCSGCTGVGRC 27
 RESULT 14
 AAY43724
 ID AAY43724 standard; peptide: 27 AA.
 AC AAY43724;
 XX 11-FEB-2000 (first entry)
 XX Amino acid sequence of an omega-conotoxin derivative of CVID.
 DE Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 XX neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX Synthetic.

OS Conus catus.
 XX WO9954350-A1.
 XX 28-OCT-1999.
 XX 16-APR-1999; 99WO-AU00288.
 XX 16-APR-1998; 98AU-0002989.
 PR 01-FEB-1999; 99AU-0008419.
 XX (UYQU) UNIV QUEENSLAND.
 XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX WPI; 2000-013226/01.
 XX Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -
 XX Claim 6; Page 45; 81pp; English.
 XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, and diseases which cause
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.
 XX Sequence 27 AA;
 SQ Query Match 96.2%; Score 152; DB 21; Length 27;
 Best Local Similarity 96.3%; Pred. NO. 2.8e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CKSKGAKCSKLMYDCSCSGCTGVGRC 27
 DB 1 CKSKGAKCSKLMYDCSCSGCTGVGRC 27
 RESULT 15
 AAY43726
 ID AAY43726 standard; peptide: 27 AA.
 AC AAY43726;
 XX 11-FEB-2000 (first entry)
 XX Amino acid sequence of an omega-conotoxin derivative of CVID.
 DE Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX Synthetic.
 OS Conus catus.
 XX Key Location/Qualifiers ,
 FT Misc-difference 5 /note= "D-form residue"
 FT
 XX WO9954350-A1.
 XX 28-OCT-1999.
 XX 16-APR-1999; 99WO-AU00288.

XX 16-APR-1998; 98AU-0002989.
 PR 01-FEB-1999; 99AU-0008419.
 XX
 PA (UYQU) UNIV QUEENSLAND.
 XX
 XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX WPI: 2000-013226/01.
 XX
 PT Novel peptides used for the treatment of disorders and diseases where
 XX blockage of the N-type calcium channels is required -
 XX
 PS Claim 6; Page 45; 81pp; English.
 XX
 CC AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.
 XX

SQ Sequence 27 AA;

Query Match 96.2%; Score 152; DB 21; Length 27;
 Best Local Similarity 96.3%; Pred. No. 2.8e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKSKGAKCSKLMYDCSCSGSGTVGRC 27
 |||||
 Db 1 CKSRAAKCSKLMYDCSCSGSGTVGRC 27

Search completed: February 26, 2003, 08:36:51
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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:39:54 : Search time 3.84615 Seconds
(without alignments)
58.846 Million cell updates/sec

Title: US-09-673-490B-2
Perfect score: 31
Sequence: 1 SKLMYD 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174566 seqs, 37721826 residues
Total number of hits satisfying chosen parameters: 174566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	27	87.1	352	9	US-09-738-626-5822
3	27	87.1	773	10	US-09-815-242-11330
4	26	83.9	319	9	US-09-884-767A-215
5	26	83.9	424	9	US-09-884-767A-213
6	26	83.9	432	10	US-09-809-517A-25
7	26	83.9	434	10	US-09-809-517A-23
8	26	83.9	434	10	US-09-809-517A-26
9	26	83.9	518	10	US-09-918-171A-22
10	26	83.9	930	10	US-09-918-171A-22
11	25	80.6	80	10	US-09-864-761-34330
12	25	80.6	88	10	US-09-751-100B-64
13	25	80.6	218	12	US-10-011-033-2
14	25	80.6	218	12	US-10-011-033-4
15	25	80.6	218	12	US-10-011-033-6
16	25	80.6	218	12	US-10-011-033-12
17	25	80.6	218	12	US-10-011-033-13
18	25	80.6	218	12	US-10-011-033-15
19	25	80.6	266	10	US-09-815-242-11580

20	25	80.6	288	9	US-10-016-668-6	Sequence 6, Appli
21	25	80.6	348	9	US-09-764-868-1073	Sequence 1073, Ap
22	25	80.6	348	9	US-09-955-999-101	Sequence 101, App
23	25	80.6	360	10	US-09-925-301-1068	Sequence 1068, Ap
24	25	80.6	364	10	US-09-775-879-15	Sequence 15, Appl
25	25	80.6	425	10	US-09-815-242-11398	Sequence 11398, A
26	25	80.6	529	9	US-09-258-031B-16	Sequence 16, Appl
27	25	80.6	529	9	US-09-258-031B-20	Sequence 20, Appl
28	25	80.6	1031	9	US-09-764-868-647	Sequence 647, App
29	25	80.6	1294	12	US-10-071-223-2	Sequence 2, Appli
30	25	80.6	1353	10	US-09-751-100B-2	Sequence 2, Appli
31	25	80.6	1353	10	US-09-751-100B-99	Sequence 99, Appl
32	25	80.6	1353	12	US-10-071-223-3	Sequence 3, Appli
33	24	77.4	27	10	US-09-864-761-45893	Sequence 45893, A
34	24	77.4	118	10	US-09-867-550-1670	Sequence 1670, Ap
35	24	77.4	126	9	US-09-738-626-5169	Sequence 5169, Ap
36	24	77.4	253	9	US-09-853-450-4	Sequence 4, Appli
37	24	77.4	255	9	US-09-853-450-6	Sequence 6, Appli
38	24	77.4	273	9	US-09-991-496-83	Sequence 83, Appl
39	24	77.4	273	10	US-09-874-923-83	Sequence 83, Appl
40	24	77.4	416	10	US-09-801-368-54	Sequence 54, Appl
41	24	77.4	421	10	US-09-793-306-163	Sequence 163, App
42	24	77.4	431	9	US-09-893-519A-26	Sequence 26, Appl
43	24	77.4	433	10	US-09-815-242-10877	Sequence 10877, A
44	24	77.4	722	10	US-09-815-242-10494	Sequence 10494, A
45	24	77.4	903	10	US-09-905-983-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-09-764-887-221
; Sequence 221, Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA113
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (18)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-764-887-221

Query Match 87.1%; Score 27; DB 10; Length 67;
Best Local Similarity 100.0%; Pred.No.12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KLMYD 6
Db 28 KLMYD 32
RESULT 2
US-09-738-626-5822
; Sequence 5822, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI

```

; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5822
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
3-09-738-626-5822

Query Match      87.1%; Score 27; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SKLMDYD 6
   |||||
Db 91 KLMYD 95

RESULT 3
US-09-815-242-11330
; Sequence 11330, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11330
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Helicobacter pylori

Query Match      87.1%; Score 27; DB 9; Length 773;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMDYD 6
   |||||
Db 348 SKLVDYD 353

US-09-884-767A-215
; Sequence 215, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 215
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage M13mp18
US-09-884-767A-215

Query Match      83.9%; Score 26; DB 9; Length 319;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SKLMDYD 6
   |||||
Db 86 SKAMVD 91

US-09-884-767A-213
; Sequence 213, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 213
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage M13mp18
US-09-884-767A-213

Query Match      83.9%; Score 26; DB 9; Length 424;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 SKLMYD 6
|||
Db 191 SKAMVD 196

RESULT 6

US-09-809-517A-25
; Sequence 25, Application US/09809517A
; Patent No. US20020034733A1
; GENERAL INFORMATION:
; APPLICANT: Lohning, Corinna
; TITLE OF INVENTION: No. US20020034733A1 methods for displaying (poly)peptides/prote
; FILE OF INVENTION: particles via disulfide bonds
; FILE REFERENCE: MORPHO/11
; CURRENT APPLICATION NUMBER: US/09/809,517A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 432
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-25

Query Match 83.9%; Score 26; DB 10; Length 432;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLMYD 6
|||
Db 199 SKAMVD 204

RESULT 7

US-09-809-517A-23
; Sequence 23, Application US/09809517A
; Patent No. US20020034733A1
; GENERAL INFORMATION:
; APPLICANT: Lohning, Corinna
; TITLE OF INVENTION: No. US20020034733A1 methods for displaying (poly)peptides/prote
; FILE OF INVENTION: particles via disulfide bonds
; FILE REFERENCE: MORPHO/11
; CURRENT APPLICATION NUMBER: US/09/809,517A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 434
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-23

Query Match 83.9%; Score 26; DB 10; Length 434;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLMYD 6
|||
Db 201 SKAMVD 206

RESULT 8

US-09-809-517A-26
; Sequence 26, Application US/09809517A
; Patent No. US20020034733A1
; GENERAL INFORMATION:
; APPLICANT: Lohning, Corinna
; TITLE OF INVENTION: No. US20020034733A1 methods for displaying (poly)peptides/pr
; FILE OF INVENTION: particles via disulfide bonds
; FILE REFERENCE: MORPHO/11
; CURRENT APPLICATION NUMBER: US/09/809,517A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 434
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-26

Query Match 83.9%; Score 26; DB 10; Length 434;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLMYD 6
|||
Db 201 SKAMVD 206

RESULT 9

US-09-918-171A-22
; Sequence 22, Application US/09918171A
; Patent No. US2002010894A1
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/04193
; CURRENT APPLICATION NUMBER: US/09/918,171A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/369,364
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-5
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (99)
; OTHER INFORMATION: xaa = Met
US-09-918-171A-22

Query Match 83.9%; Score 26; DB 10; Length 518;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLMYD 6
|||
Db 302 SKLOYD 307

RESULT 10

US-09-918-171A-2
; Sequence 2, Application US/09918171A

; Patent No. US20020110894A1
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/04193
; CURRENT APPLICATION NUMBER: US/09/918,171A
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/369,364
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 930
; TYPE: PRT
; ORGANISM: mus musculus ADAMTS-5
US-09-918-171A-2

Query Match 83.9%; Score 26; DB 10; Length 930;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 SKLQYD 6
||| ||
Db 714 SKLQYD 719

RESULT 11
US-09-864-761-34330
; Sequence 34330, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34330
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008174.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
US-09-864-761-34330

Query Match 80.6%; Score 25; DB 10; Length 80;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SKLQYD 6
||| ||
Db 5 SKLQYD 10

RESULT 12
US-09-751-100B-64
; Sequence 64, Application US/09751100B
; Patent No. US20020142436A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Human Adenylate Cyclase and Use Therefor
; FILE REFERENCE: P27948A
; CURRENT APPLICATION NUMBER: US/09/751,100B
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer based on mouse adenyl cyclase 9
US-09-751-100B-64

Query Match 80.6%; Score 25; DB 10; Length 88;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLQYD 6
||| ||
Db 75 TKLLYD 80

RESULT 13
US-10-011-033-2
; Sequence 2, Application us/10011033
; Patent No. US20020124286A1
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; McMaster, J. Russell
; Tricoli, David M
; Reynolds, John F
; Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; Cucumber Mosaic Virus

```

;
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,033
; FILING DATE: 13-NO. US20020124286A1-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
;
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-011-033-2

Query Match 80.6%; Score 25; DB 12; Length 218;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
Db 164 NKLLYD 169
:|:|:|

RESULT 14
US-10-011-033-4
; Sequence 4, Application US/10011033
; Patent No. US20020124286A1
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; McMaster, J. Russell
; Tricoli, David M
; Reynolds, John F
; Carney, Kim J
;
; TITLE OF INVENTION: Plants Resistant to C Strains of
; Cucumber Mosaic Virus
;
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,033
; FILING DATE: 13-NO. US20020124286A1-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:

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;
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-011-033-4

Query Match 80.6%; Score 25; DB 12; Length 218;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
Db 164 NKLLYD 169
:|:|:|

RESULT 15
US-10-011-033-6
; Sequence 6, Application US/10011033
; Patent No. US20020124286A1
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; McMaster, J. Russell
; Tricoli, David M
; Reynolds, John F
; Carney, Kim J
;
; TITLE OF INVENTION: Plants Resistant to C Strains of
; Cucumber Mosaic Virus
;
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,033
; FILING DATE: 13-NO. US20020124286A1-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-011-033-6

Query Match 80.6%; Score 25; DB 12; Length 218;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;

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Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMD 6

:||:|

Db 164 NKLLD 169

Search completed: February 26, 2003, 08:52:59
Job time : 3.84615 secs

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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:35:20 ; Search time 5.23077 Seconds
(without alignments)
33.750 Million cell updates/sec

Title: US-09-673-490B-2
Perfect score: 31
Sequence: 1 SKLMD 6

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTOUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	90.3	13	6	Patent No. 5189020
2	28	90.3	13	6	5424218-11
3	28	90.3	16	6	Patent No. 5424218
4	28	90.3	16	6	Patent No. 5189020-13
5	28	90.3	16	6	Patent No. 5189020-15
6	28	90.3	16	6	Patent No. 5189020-16
7	28	90.3	16	6	Patent No. 5424218
8	28	90.3	16	6	Patent No. 5424218-15
9	28	90.3	25	1	US-07-789-913-1
10	28	90.3	25	1	US-07-789-913-9
11	28	90.3	25	1	US-07-789-913-10
12	28	90.3	25	1	US-07-789-913-13
13	28	90.3	25	1	US-07-789-913-16
14	28	90.3	25	1	US-07-789-913-17
15	28	90.3	25	1	US-08-049-794-1
16	28	90.3	25	1	US-08-049-794-9
17	28	90.3	25	1	US-08-049-794-10
18	28	90.3	25	1	US-08-049-794-16
19	28	90.3	25	1	US-08-049-794-17
20	28	90.3	25	1	US-08-496-847-1
21	28	90.3	25	1	US-08-496-847-9
22	28	90.3	25	1	US-08-496-847-10
23	28	90.3	25	1	US-08-496-847-16
24	28	90.3	25	1	US-08-496-847-17
25	28	90.3	25	2	US-08-742-774-1
26	28	90.3	25	2	US-08-742-774-9
27	28	90.3	25	2	US-08-742-774-10

ALIGNMENTS

RESULT 1
5189020-11
; Patent No. 5189020
; APPLICANT: Miljanich, George P.; Bitner, Robert S.; Bowersox, Stephen S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald H.; Tsubokawa, Makoto
; TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING OMEGA CONOTOXIN PEPTIDES
; NUMBER OF SEQUENCES: 29
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,094
; FILING DATE: 22-NOV-1989
; SEQ ID NO: 11:
; LENGTH: 13
5189020-11

Query Match 90.3%; Score 28; DB 6; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	SKLMD 6
DB	2	SRLMD 7

RESULT 2
5424218-11
; Patent No. 5424218
; APPLICANT: MILJANICH, GEORGE P.; BITNER, ROBERT S.; BOWERSOX, STEPHEN S.; FOX, JAMES A.; VALENTINO, KAREN L.; YAMASHIRO, DONALD H.
; TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,714
; FILING DATE: 04-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 855,269
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: 561,766
; FILING DATE: 02-AUG-1990
; APPLICATION NUMBER: 440,094
; FILING DATE: 22-NOV-1989
; SEQ ID NO: 11:
; LENGTH: 13
5424218-11

Query Match 90.3%; Score 28; DB 6; Length 13;

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Best Local Similarity 83.3%; Pred. No. 1.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMD 6
   1:||||
Db 2 SRLMD 7

RESULT 3
5189020-13
; Patent No. 5189020
; APPLICANT: Milijanich, George P.; Bitner, Robert S.; Bowersox,
; Stephen S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald
; H.; Tsubokawa, Makoto
; TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING
; OMEGA CONOTOXIN PEPTIDES
; NUMBER OF SEQUENCES: 29
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,094
; FILING DATE: 22-NOV-1989
EQ ID NO:13:
LENGTH: 16
5189020-13

Query Match 90.3%; Score 28; DB 6; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMD 6
   1:||||
Db 9 SRLMD 14

RESULT 4
5189020-15
; Patent No. 5189020
; APPLICANT: Milijanich, George P.; Bitner, Robert S.; Bowersox,
; Stephen S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald
; H.; Tsubokawa, Makoto
; TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING
; OMEGA CONOTOXIN PEPTIDES
; NUMBER OF SEQUENCES: 29
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,094
; FILING DATE: 22-NOV-1989
EQ ID NO:15:
LENGTH: 16
5189020-15

Query Match 90.3%; Score 28; DB 6; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMD 6
   1:||||
Db 9 SRLMD 14

RESULT 5
5189020-16
; Patent No. 5189020
; APPLICANT: Milijanich, George P.; Bitner, Robert S.; Bowersox,
; Stephen S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald
; H.; Tsubokawa, Makoto
; TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING
; OMEGA CONOTOXIN PEPTIDES
; NUMBER OF SEQUENCES: 29
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,094
; FILING DATE: 22-NOV-1989
EQ ID NO:16:
LENGTH: 16
5189020-16

Query Match 90.3%; Score 28; DB 6; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMD 6
   1:||||
Db 9 SRLMD 14

RESULT 6
5424218-13
; Patent No. 5424218
; APPLICANT: Miljanich, George P.; Bitner, Robert S.; Bowersox,
; Stephen S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald H.
; TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,714
; FILING DATE: 04-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 855,269
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: 561,766
; FILING DATE: 02-AUG-1990
; APPLICATION NUMBER: 440,094
; FILING DATE: 22-NOV-1989
; SEQ ID NO:13:
; LENGTH: 16
5424218-13

Query Match 90.3%; Score 28; DB 6; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMD 6
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Db 9 SRLMD 14

RESULT 7
5424218-15
; Patent No. 5424218
; APPLICANT: Miljanich, George P.; Bitner, Robert S.; Bowersox,
; Stephen S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald H.
; TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,714
; FILING DATE: 04-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 855,269
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: 561,766
; FILING DATE: 02-AUG-1990
; APPLICATION NUMBER: 440,094
; FILING DATE: 22-NOV-1989
; SEQ ID NO:15:
; LENGTH: 16
5424218-15

Query Match 90.3%; Score 28; DB 6; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SKLMD 6
I:||||
Db 9 SRLMD 14

RESULT 8
5424218-16
Patent No. 5424218
APPLICANT: MILJANICH, GEORGE P.; BITNER, ROBERT S.; BOWERSOX,
STEPHEN S.; FOX, JAMES A.; VALENTINO, KAREN L.; YAMASHIRO, DONALD H.
TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
FILING DATE: 04-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 855,269
FILING DATE: 23-MAR-1992
APPLICATION NUMBER: 561,766
FILING DATE: 02-AUG-1990
APPLICATION NUMBER: 440,094
FILING DATE: 22-NOV-1989
SEQ ID NO: 16:
LENGTH: 16
5424218-16

Query Match 90.3%; Score 28; DB 6; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMD 6
I:||||
Db 9 SRLMD 14

RESULT 9
US-07-789-913-1
Sequence 1, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Bitner, Robert S.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing
Ischemia-Related Neuronal Damage
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids

NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-111
US-07-789-913-1

Query Match 90.3%; Score 28; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMD 6
I:||||
Db 9 SRLMD 14

RESULT 10
US-07-789-913-9
Sequence 9, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Bitner, Robert S.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing
Ischemia-Related Neuronal Damage
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids

TYPE: AMINO ACID
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-190
US-07-789-913-9

Query Match 90.3%; Score 28; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
1:||||
Db 9 SRLMYD 14

RESULT 11

US-07-789-913-10
; Sequence 10, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:

APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Bitner, Robert S.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing
TITLE OF INVENTION: Ischemia-Related Neuronal Damage
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07789,913

FILING DATE: 19911112

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/561,766

FILING DATE: 02-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/440,094

FILING DATE: 22-NOV-1989

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0005.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: AMINO ACID

TOPOLOGY: both

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: SNX-191

US-07-789-913-10

Query Match 90.3%; Score 28; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
1:||||
Db 9 SRLMYD 14

RESULT 12

US-07-789-913-13

; Sequence 13, Application US/07789913

; Patent No. 5559095

; GENERAL INFORMATION:

APPLICANT: Miljanich, George P.

APPLICANT: Bowersox, Stephen S.

APPLICANT: Fox, James A.

APPLICANT: Valentino, Karen L.

APPLICANT: Bitner, Robert S.

APPLICANT: Yamashiro, Donald H.

TITLE OF INVENTION: Delayed Treatment Method of Reducing

TITLE OF INVENTION: Ischemia-Related Neuronal Damage

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Peter Dehlinger

STREET: 350 Cambridge Avenue, Suite 300

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07789,913

FILING DATE: 19911112

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/561,766

FILING DATE: 02-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/440,094

FILING DATE: 22-NOV-1989

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0005.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: AMINO ACID

TOPOLOGY: both

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: SNX-195

US-07-789-913-13

Query Match 90.3%; Score 28; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
1:||||
Db 9 SRLMYD 14

RESULT 13

US-07-789-913-16
; Sequence 16, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,913
; FILING DATE: 19911112
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; FILING DATE: 22-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0005.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-198

US-07-789-913-16

Query Match 90.3%; Score 28; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
; 1:|||||
Db 9 SRLMYD 14

RESULT 14

US-07-789-913-17
; Sequence 17, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.

; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,913
; FILING DATE: 19911112
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; FILING DATE: 22-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0005.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-200

US-07-789-913-17

Query Match 90.3%; Score 28; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
; 1:|||||
Db 9 SRLMYD 14

RESULT 15

US-08-049-794-1
; Sequence 1, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA

; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA

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; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 19930415
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVLIA/SNX-111, FIGURE 1
; US-08-049-794-1

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Query Match          90.3%; Score 28; DB 1; Length 25;
Best Local Similarity 89.3%; Pred. No. 2.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 SKLMYD 6
Db 9 SRLMYD 14

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Search completed: February 26, 2003, 08:41:04
Job time : 6.23077 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:30:59 ; Search time 13.5385 Seconds
(without alignments)
59.054 Million cell updates/sec

Title: US-09-673-490B-2

Perfect score: 31

Sequence: 1 SKLMYD 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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20: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	6	21 AAY43708	Sequence of the se
2	31	100.0	27	21 AAY43711	Amino acid sequenc
3	31	100.0	27	21 AAY43718	Amino acid sequenc
4	31	100.0	27	21 AAY43719	Amino acid sequenc
5	31	100.0	27	21 AAY43720	Amino acid sequenc
6	31	100.0	27	21 AAY43721	Amino acid sequenc
7	31	100.0	27	21 AAY43725	Amino acid sequenc
8	31	100.0	27	21 AAY43726	Amino acid sequenc
9	31	100.0	27	21 AAY43728	Amino acid sequenc
10	31	100.0	28	21 AAY43727	Amino acid sequenc

11	31	100.0	28	21 AAY43729	Amino acid sequenc
12	31	100.0	28	21 AAY43730	Amino acid sequenc
13	31	100.0	73	21 AAY43717	Amino acid sequenc
14	29	93.5	1523	22 AAG84955	Shrimp white spot
15	28	90.3	6	21 AAY43709	Sequence of the se
16	28	90.3	13	14 AAR32787	MVIIA omega conoto
17	28	90.3	13	16 AAR76099	Omega conotoxin MV
18	28	90.3	16	14 AAR32789	MVIIA omega conoto
19	28	90.3	16	14 AAR32791	MVIIA omega conoto
20	28	90.3	16	14 AAR32792	MVIIA omega conoto
21	28	90.3	16	16 AAR76101	Omega conotoxin MV
22	28	90.3	16	16 AAR76103	Omega conotoxin MV
23	28	90.3	16	16 AAR76104	Omega conotoxin MV
24	28	90.3	25	12 AAR12544	Omega conotoxin pe
25	28	90.3	25	12 AAR12545	Omega conotoxin pe
26	28	90.3	25	12 AAR13264	Omega conotoxin pe
27	28	90.3	25	14 AAR32777	MVIIA omega conoto
28	28	90.3	25	14 AAR32752	MVIIA/SNX-111. Sy
29	28	90.3	25	14 AAR37763	SNX-191. Syntheti
30	28	90.3	25	14 AAR37764	SNX-191. Syntheti
31	28	90.3	25	14 AAR37767	SNX-195. Syntheti
32	28	90.3	25	14 AAR37770	SNX-198. Syntheti
33	28	90.3	25	14 AAR37771	SNX-200. Syntheti
34	28	90.3	25	14 AAR39608	MVIIA/SNX111. Syn
35	28	90.3	25	14 AAR39625	SNX-198. Syntheti
36	28	90.3	25	14 AAR39626	SNX-200. Syntheti
37	28	90.3	25	14 AAR39618	SNX-190. Syntheti
38	28	90.3	25	14 AAR39619	SNX-191. Syntheti
39	28	90.3	25	14 AAR39620	SNX-193. Syntheti
40	28	90.3	25	14 AAR39622	SNX-196. Syntheti
41	28	90.3	25	14 AAR39623	Omega conotoxin MV
42	28	90.3	25	16 AAR76089	SNX-195, omega con
43	28	90.3	25	18 AAW19559	SNX-198, omega con
44	28	90.3	25	18 AAW19562	SNX-200, omega con
45	28	90.3	25	18 AAW19564	

ALIGNMENTS

RESULT 1

AAY43708

ID AAY43708 standard; peptide; 6 AA.

XX AC AAY43708;

XX DT 11-FEB-2000 (first entry)

XX DE Sequence of the second loop of an omega conotoxin.

XX KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;
KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX OS Conus magus.

XX PN WO954350-A1.

XX PD 28-OCT-1999.

XX PF 16-APR-1999; 99WO-AU00288.

XX PR 16-APR-1998; 98AU-0002989.

XX PR 01-FEB-1999; 99AU-0008419.

XX PA (UYQU) UNIV QUEENSLAND.

XX PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX DR WPI; 2000-013226/01.

XX PT Novel peptides used for the treatment of disorders and diseases where

PT blockage of the N-type calcium channels is required -

PS Claim 5; Page 45; 81pp; English.

CC The present sequence represents the second loop of an isolated, synthetic, or recombinant omega-conotoxin. Omega-conotoxins are isolated from venoms of predatory marine snails, and have a selectivity for N-type calcium channels over P/Q type channels, and so block N-type calcium channels. The omega-conotoxins of the invention can be used in any disease or disorder where blockage of N-type calcium channels is required, e.g. in the reduction of neuronal damage following ischemia, production of analgesia, or enhancement of opiate analgesia, in the treatment of schizophrenia, stimulant induced psychoses, hypertension, inflammation, and diseases which cause bronchotension, and also in the inhibition of progression of neuropathic pain. They can also be used in a screen to identify compounds with activity at N-type voltage sensitive calcium channels.

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 21; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6

Db 1 SKLMYD 6

RESULT 2

AA43711

ID AAY43711 standard; peptide: 27 AA.

AC AAY43711;

XX

XX

DT 11-FEB-2000 (first entry)

XX

DE Amino acid sequence of an omega-conotoxin CVID.

XX

KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel; neuronal damage reduction; ischemia; analgesia; opiate analgesia;

KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;

KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX

OS Conus catus.

XX

PN W09954350-A1.

XX

PD 28-OCT-1999.

XX

PF 16-APR-1999; 99WO-AU00288.

XX

PR 16-APR-1998; 98AU-0002989.

PR 01-FEB-1999; 99AU-0008419.

XX

PA (UYQU) UNIV QUEENSLAND.

XX

PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX

DR WPI: 2000-013226/01.

XX

PT Novel peptides used for the treatment of disorders and diseases where blockage of the N-type calcium channels is required -

PS Claim 6; Page 45; 81pp; English.

CC The present sequence represents an omega-conotoxin. Omega-conotoxins are isolated from venoms of predatory marine snails, and have a selectivity for N-type calcium channels over P/Q type channels, and so block N-type calcium channels. The omega-conotoxins of the invention can be used in any disease or disorder where blockage of N-type calcium channels is required, e.g. in the reduction of neuronal damage following ischemia, production of analgesia, or enhancement of opiate analgesia,

CC in the treatment of schizophrenia, stimulant induced psychoses, hypertension, inflammation, and diseases which cause bronchotension, and also in the inhibition of progression of neuropathic pain. They can also be used in a screen to identify compounds with activity at N-type voltage sensitive calcium channels.

XX

SQ Sequence 27 AA;

Query Match 100.0%; Score 31; DB 21; Length 27;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6

Db 9 SKLMYD 14

RESULT 3

AA43718

ID AAY43718 standard; peptide: 27 AA.

AC AAY43718;

XX

XX

DT 11-FEB-2000 (first entry)

XX

DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX

KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel; neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;

KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;

KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX

OS Synthetic.

OS Conus catus.

XX

PN W09954350-A1.

XX

PD 28-OCT-1999.

XX

PF 16-APR-1999; 99WO-AU00288.

XX

PR 16-APR-1998; 98AU-0002989.

PR 01-FEB-1999; 99AU-0008419.

XX

PA (UYQU) UNIV QUEENSLAND.

XX

PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX

DR WPI: 2000-013226/01.

XX

PT Novel peptides used for the treatment of disorders and diseases where blockage of the N-type calcium channels is required -

PS Claim 6; Page 45; 81pp; English.

XX

AA43718-36 represent derivatives of omega-conotoxin CVID.

CC Omega-conotoxins are isolated from venoms of predatory marine snails, and have a selectivity for N-type calcium channels over P/Q type channels, and so block N-type calcium channels. The omega-conotoxins of the invention can be used in any disease or disorder where blockage of N-type calcium channels is required, e.g. in the reduction of neuronal damage following ischemia, production of analgesia, or enhancement of opiate analgesia, in the treatment of schizophrenia, stimulant induced psychoses, hypertension, inflammation, and diseases which cause bronchotension, and also in the inhibition of progression of neuropathic pain. They can also be used in a screen to identify compounds with activity at N-type voltage sensitive calcium channels.

XX

SQ Sequence 27 AA;

Query Match 100.0%; Score 31; DB 21; Length 27;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
 DT |||||
 Db 9 SKLMYD 14

RESULT 4

AAAY43719
 ID AAY43719 standard; peptide: 27 AA.

XX AC AAY43719;

XX DT 11-FEB-2000 (first entry)

XX DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX OS Synthetic.

XX OS Conus catus.

XX PN WO9954350-A1.

XX PD 28-OCT-1999.

XX PF 16-APR-1999; 99WO-AU00288.

XX PR 16-APR-1998; 98AU-0002989.

XX PR 01-FEB-1999; 99AU-0008419.

XX PA (UYQU) UNIV QUEENSLAND.

XX PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX DR WPI; 2000-013226/01.

XX PT Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -

XX PS Claim 6; Page 45; 81pp; English.

XX CC AAY43718-36 represent derivatives of omega-conotoxin CVID.

CC CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC calcium channels can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.

XX SQ Sequence 27 AA;

Query Match 100.0%; Score 31; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
 DT |||||
 Db 9 SKLMYD 14

RESULT 5

AAAY43720
 ID AAY43720 standard; peptide: 27 AA.

XX AC AAY43720;

XX 11-FEB-2000 (first entry)

XX DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX OS Synthetic.

XX OS Conus catus.

XX PN WO9954350-A1.

XX PD 28-OCT-1999.

XX PF 16-APR-1999; 99WO-AU00288.

XX PR 16-APR-1998; 98AU-0002989.

XX PR 01-FEB-1999; 99AU-0008419.

XX PA (UYQU) UNIV QUEENSLAND.

XX PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX DR WPI; 2000-013226/01.

XX PT Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -

XX PS Claim 6; Page 45; 81pp; English.

XX CC AAY43718-36 represent derivatives of omega-conotoxin CVID.

CC CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC calcium channels can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.

XX SQ Sequence 27 AA;

Query Match 100.0%; Score 31; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
 DT |||||
 Db 9 SKLMYD 14

RESULT 6

AAAY43721
 ID AAY43721 standard; peptide: 27 AA.

XX AC AAY43721;

XX DT 11-FEB-2000 (first entry)

XX DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX OS Synthetic.

OS Conus catus.
 XX WO9954350-A1.
 XX 28-OCT-1999.
 XX 16-APR-1999; 99WO-AU00288.
 XX 16-APR-1998; 98AU-0002989.
 PR 01-FEB-1999; 99AU-0008419.
 XX (UYQU) UNIV QUEENSLAND.
 XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX WPI; 2000-013226/01.
 XX Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -
 XX Claim 6; Page 45; 81pp; English.
 XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.
 XX SQ Sequence 27 AA;
 Query Match 100.0%; Score 31; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SKLMYD 6
 Db 9 SKLMYD 14
 RESULT 7
 AAY43725
 ID AAY43725 standard; peptide; 27 AA.
 AC AAY43725;
 XX 11-FEB-2000 (first entry)
 DT Amino acid sequence of an omega-conotoxin derivative of CVID.
 DE Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 XX neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX Synthetic.
 OS Conus catus.
 OS Key Location/Qualifiers
 FT Misc-difference 5 /note= "D-form residue"
 FT WO9954350-A1.
 XX 28-OCT-1999.
 XX 16-APR-1999; 99WO-AU00288.
 XX 16-APR-1998; 98AU-0002989.
 PR 01-FEB-1999; 99AU-0008419.
 XX (UYQU) UNIV QUEENSLAND.
 XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX WPI; 2000-013226/01.
 XX Novel peptides used for the treatment of disorders and diseases where

PA (UYQU) UNIV QUEENSLAND.
 XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX WPI; 2000-013226/01.
 XX Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -
 XX Claim 6; Page 45; 81pp; English.
 XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.
 XX SQ Sequence 27 AA;
 Query Match 100.0%; Score 31; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SKLMYD 6
 Db 9 SKLMYD 14
 RESULT 8
 AAY43726
 ID AAY43726 standard; peptide; 27 AA.
 AC AAY43726;
 XX 11-FEB-2000 (first entry)
 DT Amino acid sequence of an omega-conotoxin derivative of CVID.
 DE Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 XX neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX Synthetic.
 OS Conus catus.
 OS Key Location/Qualifiers
 FT Misc-difference 5 /note= "D-form residue"
 FT WO9954350-A1.
 XX 28-OCT-1999.
 XX 16-APR-1999; 99WO-AU00288.
 XX 16-APR-1998; 98AU-0002989.
 PR 01-FEB-1999; 99AU-0008419.
 XX (UYQU) UNIV QUEENSLAND.
 XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX WPI; 2000-013226/01.
 XX Novel peptides used for the treatment of disorders and diseases where

PT blockage of the N-type calcium channels is required -
 XX Claim 6; Page 45; 81pp; English.
 CC AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.
 XX Sequence 27 AA;
 SQ

Query Match 100.0%; Score 31; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMD 6
 Db 9 SKLMD 14
 |||||

RESULT 9
 AAY43728
 ID AAY43728 standard; peptide; 27 AA.
 XX
 AC AAY43728;
 DT 11-FEB-2000 (first entry)
 XX
 DE Amino acid sequence of an omega-conotoxin derivative of CVID.
 XX
 KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX
 OS Synthetic.
 OS Conus catus.
 FH Key Location/Qualifiers
 FT Misc-difference 27 /note= "free carboxyl at the C-terminal"
 FT
 XX
 PN WO9954350-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 16-APR-1999; 99WO-AU00288.
 XX
 PR 16-APR-1998; 98AU-0002989.
 PR 01-FEB-1999; 99AU-0008419.
 XX
 PA (UYQU) UNIV QUEENSLAND.
 XX
 PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX
 DR WPI; 2000-013226/01.
 XX
 PF Novel peptides used for the treatment of disorders and diseases where
 XX blockage of the N-type calcium channels is required -
 XX
 PR Claim 6; Page 45; 81pp; English.
 XX
 PA AAY43718-36 represent derivatives of omega-conotoxin CVID.
 XX
 PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX
 DR WPI; 2000-013226/01.
 XX
 PF Novel peptides used for the treatment of disorders and diseases where
 XX blockage of the N-type calcium channels is required -
 XX
 PR Claim 6; Page 45; 81pp; English.
 XX
 PA AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.
 XX Sequence 28 AA;
 SQ

CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.
 XX Sequence 27 AA;
 SQ

Query Match 100.0%; Score 31; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMD 6
 Db 9 SKLMD 14
 |||||

RESULT 10
 AAY43727
 ID AAY43727 standard; peptide; 28 AA.
 XX
 AC AAY43727;
 DT 11-FEB-2000 (first entry)
 XX
 DE Amino acid sequence of an omega-conotoxin derivative of CVID.
 XX
 KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX
 OS Synthetic.
 OS Conus catus.
 PN WO9954350-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 16-APR-1999; 99WO-AU00288.
 XX
 PR 16-APR-1998; 98AU-0002989.
 PR 01-FEB-1999; 99AU-0008419.
 XX
 PA (UYQU) UNIV QUEENSLAND.
 XX
 PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX
 DR WPI; 2000-013226/01.
 XX
 PF Novel peptides used for the treatment of disorders and diseases where
 XX blockage of the N-type calcium channels is required -
 XX
 PR Claim 6; Page 45; 81pp; English.
 XX
 PA AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.
 XX Sequence 28 AA;
 SQ

Query Match 100.0%; Score 31; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMD 6
Db 9 SKLMD 14

RESULT 11

AA43729
ID AAY43729 standard; peptide; 28 AA.

XX AC AAY43729;
XX DT 11-FEB-2000 (first entry)
XX DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
XX KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
XX KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
XX KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX OS Synthetic.
XX OS Conus catus.
XX PN WO9954350-A1.
XX PD 28-OCT-1999.

XX PF 16-APR-1999; 99WO-AU00288.
XX PR 16-APR-1998; 98AU-0002989.
XX PR 01-FEB-1999; 99AU-0008419.

XX PA (UYQU) UNIV QUEENSLAND.

XX PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX WPI: 2000-013226/01.

XX PT Novel peptides used for the treatment of disorders and diseases where
XX PT blockage of the N-type calcium channels is required -

XX PS Claim 6; Page 46; 81pp; English.

XX CC AAY43718-36 represent derivatives of omega-conotoxin CVID.
XX CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
XX CC have a selectivity for N-type calcium channels over P/Q type channels,
XX CC and so block N-type calcium channels. The omega-conotoxins of the
XX CC invention can be used in any disease or disorder where blockage of N-type
XX CC calcium channels is required, e.g. in the reduction of neuronal damage
XX CC following ischemia, production of analgesia, or enhancement of opiate
XX CC analgesia, in the treatment of schizophrenia, stimulant induced
XX CC psychoses, hypertension, inflammation, and diseases which cause
XX CC bronchotension, and also in the inhibition of progression of neuropathic
XX CC pain. They can also be used in a screen to identify compounds with
XX CC activity at N-type voltage sensitive calcium channels.

XX SQ Sequence 28 AA;

Query Match 100.0%; Score 31; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMD 6
Db 10 SKLMD 15

RESULT 12

AA43730
ID AAY43730 standard; peptide; 28 AA.

XX AC AAY43730;

XX DT 11-FEB-2000 (first entry)

XX DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
XX KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
XX KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
XX KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX OS Synthetic.
XX OS Conus catus.

XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "acetylated residue"

XX PN WO9954350-A1.

XX PD 28-OCT-1999.

XX PF 16-APR-1999; 99WO-AU00288.

XX PR 16-APR-1998; 98AU-0002989.

XX PR 01-FEB-1999; 99AU-0008419.

XX PA (UYQU) UNIV QUEENSLAND.

XX PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX WPI: 2000-013226/01.

XX PT Novel peptides used for the treatment of disorders and diseases where
XX PT blockage of the N-type calcium channels is required -

XX PS Claim 6; Page 46; 81pp; English.

XX CC AAY43718-36 represent derivatives of omega-conotoxin CVID.
XX CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
XX CC have a selectivity for N-type calcium channels over P/Q type channels,
XX CC and so block N-type calcium channels. The omega-conotoxins of the
XX CC invention can be used in any disease or disorder where blockage of N-type
XX CC calcium channels is required, e.g. in the reduction of neuronal damage
XX CC following ischemia, production of analgesia, or enhancement of opiate
XX CC analgesia, in the treatment of schizophrenia, stimulant induced
XX CC psychoses, hypertension, inflammation, and diseases which cause
XX CC bronchotension, and also in the inhibition of progression of neuropathic
XX CC pain. They can also be used in a screen to identify compounds with
XX CC activity at N-type voltage sensitive calcium channels.

XX SQ Sequence 28 AA;

Query Match 100.0%; Score 31; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMD 6
Db 10 SKLMD 15

RESULT 13

AA43717
ID AAY43717 standard; peptide; 73 AA.

XX AC AAY43717;

XX DT 11-FEB-2000 (first entry)

DE Amino acid sequence of an omega-conotoxin CVID.
XX
KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;
KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
XX
OS Conus catus.
XX
FH Location/Qualifiers
FT Peptide
FT 1..45
FT /note= "signal peptide"
FT Protein
FT 46..73
FT /note= "mature protein"
XX
XX WO9954350-A1.
XX
XX 28-OCT-1999.
XX
XX 16-APR-1999; 99WO-AU00288.
XX
XX 16-APR-1998; 98AU-0002989.
XX
XX 01-FEB-1999; 99AU-0008419.
XX
XX (UYQU) UNIV QUEENSLAND.
XX
XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX
XX WPI; 2000-013226/01.
XX
XX N-PSDB; AAZ30311.
XX
XX Novel peptides used for the treatment of disorders and diseases where
XX blockage of the N-type calcium channels is required .
XX
XX Disclosure; Page 60-61; 81pp; English.
XX
XX The present sequence represents an omega-conotoxin. Omega-conotoxins
XX are isolated from venoms of predatory marine snails, and have a
XX selectivity for N-type calcium channels over P/Q type channels, and so
XX block N-type calcium channels. The omega-conotoxins of the invention
XX can be used in any disease or disorder where blockage of N-type calcium
XX channels is required, e.g. in the reduction of neuronal damage following
XX ischemia, production of analgesia, or enhancement of opiate analgesia,
XX in the treatment of schizophrenia, stimulant induced psychoses,
XX hypertension, inflammation, and diseases which cause bronchotension,
XX CC and also in the inhibition of progression of neuropathic pain. They can
XX also be used in a screen to identify compounds with activity at N-type
XX voltage sensitive calcium channels.
XX
XX Sequence 73 AA;
Query Match 100.0%; Score 31; DB 21; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SKLMYD 6
Db 54 SKLMYD 59
|||||
RESULT 14
AAG84955
ID AAG84955 standard; Protein; 1523 AA.
XX
XX AAG84955;
XX
XX 11-SEP-2001 (first entry)
XX
XX Shrimp white spot Bacilliform virus (WSBV) protein 46.
XX
KW Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection;
KW antiviral agent; gene expression; antisense construct;
KW transgenic viral resistant shrimp.

XX White spot syndrome virus.
OS
XX WO200138351-A2.
PN
XX 31-MAY-2001.
PD
XX 08-NOV-2000; 2000WO-US28888.
XX
XX 24-NOV-1999; 99CN-0124717.
XX
XX (PENY-) PE CORP NY.
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOGENOMAX CO LTD.
XX
XX Xu X, Yang F, He J, Pham L, He M, Ye Y, Shen Y, Kodira C;
PI
XX WPI; 2001-355877/37.
DR
XX N-PSDB; AAH62735.
XX
XX Primary nucleotide sequence of the shrimp white spot Bacilliform virus
XX (WSBV), useful for producing viral polypeptides that can be used to
XX screen for agents that are useful for treating WSBV infection .
XX
XX Claim 1; Figure 3; 626pp; English.
XX
XX The invention provides the primary nucleotide sequence of the WSBV genome
XX (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and
XX encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences
XX (AAH62840-63160) suitable for use as primers or probes. The nucleic acid
XX molecules and proteins of the invention are useful for diagnosis and
XX monitoring viral infection, in screens for antiviral agents and for
XX monitoring viral gene expression or activity during a treatment regimen.
XX The nucleic acid molecules are also useful as antisense constructs to
XX control viral gene expression in infected cells and tissues and to create
XX transgenic viral resistant shrimp.
XX
XX Sequence 1523 AA;
Query Match 93.5%; Score 29; DB 22; Length 1523;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SKLMYD 6
Db 1330 SKIMYD 1335
|||||
RESULT 15
AAV43709
ID AAV43709 standard; peptide; 6 AA.
XX
XX AAV43709;
AC
XX 11-FEB-2000 (first entry)
DT
XX
XX Sequence of the second loop of an omega conotoxin.
XX
XX Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;
KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
XX
XX Synthetic.
OS
XX Conus catus.
OS
XX WO9954350-A1.
PN
XX 28-OCT-1999.
PD
XX
XX 16-APR-1999; 99WO-AU00288.
PF
XX 16-APR-1998; 98AU-0002989.
PR
XX 16-APR-1998; 98AU-0002989.
PR

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PR 01-FEB-1999; 99AU-0008419.
XX
XX PA (UYQU ) UNIV QUEENSLAND.
XX
XX PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX
XX DR WPI; 2000-013226/01.
XX
XX PT Novel peptides used for the treatment of disorders and diseases where
XX blockage of the N-type calcium channels is required -
XX
XX PS Claim 5; Page 45; 81pp; English.
XX
XX CC The present sequence represents the second loop of an isolated,
XX synthetic, or recombinant omega-conotoxin. Omega-conotoxins are
XX isolated from venoms of predatory marine snails, and have a
XX selectivity for N-type calcium channels over P/Q type channels, and so
XX block N-type calcium channels. The omega-conotoxins of the invention
XX can be used in any disease or disorder where blockage of N-type calcium
XX channels is required, e.g. in the reduction of neuronal damage following
XX ischemia, production of analgesia, or enhancement of opiate analgesia,
XX in the treatment of schizophrenia, stimulant induced psychoses,
XX hypertension, inflammation, and diseases which cause bronchotension,
XX and also in the inhibition of progression of neuropathic pain. They can
XX also be used in a screen to identify compounds with activity at N-type
XX voltage sensitive calcium channels.
XX
SQ Sequence 6 AA;
Query Match 90.3%; Score 28; DB 21; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.8e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 SKLMYD 6
Db 1 SRLMYD 6
Search completed: February 26, 2003, 08:36:50
Job time : 13.5385 secs

```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:32:19 ; Search time 94.1538 Seconds
(without alignments)
59.087 Million cell updates/sec

Title: US-09-673-490B-5

Perfect score: 158

Sequence: 1 CKSGAKCSKLMYDCSGSGCTVGRG 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	60.8	66	5 Q9N6F8	Q9n6f8 conus catus
2	96	60.8	66	5 Q9N6F7	Q9n6f7 conus catus
3	96	60.8	66	5 Q9N633	Q9n633 conus catus
4	96	60.8	66	5 Q9NCW6	Q9ncw6 conus catus
5	96	60.8	66	5 Q9NCW5	Q9ncw5 conus catus
6	96	60.8	66	5 Q9NCW3	Q9ncw3 conus catus
7	96	60.8	66	5 Q9NCW0	Q9ncw0 conus catus
8	96	60.8	66	5 Q9NCV9	Q9ncv9 conus catus
9	94	59.5	66	5 Q9N628	Q9n628 conus catus
10	94	59.5	66	5 Q9N625	Q9n625 conus catus
11	94	59.5	66	5 Q9NCW2	Q9ncw2 conus catus
12	93	58.9	66	5 Q9NCW1	Q9ncw1 conus catus
13	93	58.9	66	5 Q9NCV6	Q9ncv6 conus catus
14	92	58.2	66	5 Q9NCV7	Q9ncv7 conus catus
15	89	56.3	66	5 Q9NCW4	Q9ncw4 conus catus
16	89	56.3	66	5 Q9NCV5	Q9ncv5 conus catus

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17 87 55.1 66 5 Q9NCV8
18 86 54.4 66 5 Q9N6N6
19 86 54.4 66 5 Q9NCV4
20 86 54.4 66 5 Q9NCV0
21 86 54.4 66 5 Q9NCU1
22 85 53.8 66 5 Q9NCV3
23 85 53.8 66 5 Q9NCV2
24 85 53.8 66 5 Q9NCV1
25 75.5 47.8 50 12 Q8QLC7
26 68 43.0 81 5 Q9BP83
27 67.5 42.7 70 5 Q9BP80
28 64.5 40.8 52 12 Q9PYR8
29 62.5 39.6 70 5 Q9BP82
30 62.5 39.6 73 5 Q9BP79
31 58 36.7 78 5 Q9U656
32 58 36.7 78 5 Q9U655
33 57 36.1 77 5 Q9U653
34 57 36.1 77 5 Q9U652
35 57 36.1 318 10 Q9SB60
36 56 35.4 558 2 P94664
37 56 35.4 598 4 Q9G6P6
38 56 35.4 2447 5 Q9NEF9
39 56 35.4 4072 5 Q9W4Y4
40 55.5 35.1 836 6 O19057
41 55.5 35.1 2150 5 O44131
42 55 34.8 120 5 O8T507
43 55 34.8 686 5 Q94316
44 54.5 34.5 53 12 O89743
45 54.5 34.5 53 12 Q9YMH9

```

ALIGNMENTS

i

RESULT 1

```

Q9N6F8
ID Q9N6F8 PRELIMINARY; PRT; 66 AA.
AC Q9N6F8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Four-loop conotoxin precursor (fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_2_2, AND CCATH_2_1;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
   eating Conus."
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF174231; AAF89895.1; -.
DR EMBL; AF174230; AAF89894.1; -.
DR HSSP; P05484; 1MVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7109 MW; 7455A28A606AEAFD CRC64;

```

Query Match 60.8%; Score 96; DB 5; Length 66;

Best Local Similarity 59.3%; Pred No. 5.4e-07;

Matches 16; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 1 CKSGAKCSKLMYDCSGSGCTVGRG 27

I: ||| | ||| ||| |||

Db 41 CQGRGASCRKTMVNCSSGSCNR--GRC 65

RESULT 2

```

Q9N6F7
ID Q9N6F7 PRELIMINARY; PRT; 66 AA.

```

```

AC Q9NCW6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
DE
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_li_3;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AEI74216; AAF69880.1; -.
DR HSSP: P05484; LMVI.
DR InterPro: IPR004214; Conotoxin.
DR Pfam: PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7023 MW; E445339B6968B0AC CRC64;
Query Match 60.8%; Score 96; DB 5; Length 66;
Best Local Similarity 59.3%; Pred. No. 5.4e-07;
Matches 16; Conservative 2; Mismatches 7; Indels 2; G
Qy 1 CKSKGAKCKLMYDCSGSCGTGRC 27
Db 41 CKKGASCRRTSYDCTGCSRS--GRG 65

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RESULT 5
Q9NCW5 PRELIMINARY; PRT; 66 AA.
ID Q9NCW5
AC Q9NCW5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_11_4;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
RT eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; A5174217; AAF89881.1; -.
DR HSSP; P05484; IMV1.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7083 MW; E445338A7939E4A8 CRC64;

Query Match 60.8%; Score 96; DB 5; Length 66;
Best Local Similarity 59.3%; Pred. No. 5.4e-07;
Matches 16; Conservative 2; Mismatches 7; Indels 2;

QY 1 CKSKGAKSKLMYDCSGSGCSTVGRC 27
II III I : IIII:III III
Db 41 CKGKGASCRRTSYDCGTGSCRS--GRC 65

RESULT 6
Q9NCW3 PRELIMINARY; PRT; 66 AA.
ID Q9NCW3
AC Q9NCW3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

```

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
[1]

RN SEQUENCE FROM N.A.
RC STRAIN=CCATH_11_7;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-eating Conus";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174220; AAF89884.1; -.
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7054 MW; E9FE5E310968A1AC CRC64;

Query Match 60.8%; Score 96; DB 5; Length 66;
Best Local Similarity 59.3%; Pred. No. 5.4e-07;
Matches 16; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 CKSKGAKSKLMYDCCSGSGCTVGRG 27
II III I : IIII:III III
Db 41 CKRGASCRRTSYDCTGSCRS--GRC 65

RESULT 7

Q9NCW0 PRELIMINARY; PRT; 66 AA.
AC Q9NCW0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
[1]

RN SEQUENCE FROM N.A.
RC STRAIN=CCATH_2_3;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-eating Conus";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174232; AAF89896.1; -.
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7110 MW; 79EECF31006AEAFD CRC64;

Query Match 60.8%; Score 96; DB 5; Length 66;
Best Local Similarity 59.3%; Pred. No. 5.4e-07;
Matches 16; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 1 CKSKGAKSKLMYDCCSGSGCTVGRG 27
II III I : IIII:III III
Db 41 CKRGASCRRTSYDCTGSCRS--GRC 65

RESULT 8

Q9NCV9 PRELIMINARY; PRT; 66 AA.
AC Q9NCV9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=CCATH_2_4;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-eating Conus";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174233; AAF89897.1; -.
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7079 MW; 7455A29E312FEAFD CRC64;

Query Match 60.8%; Score 96; DB 5; Length 66;
Best Local Similarity 59.3%; Pred. No. 5.4e-07;
Matches 16; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 1 CKSKGAKSKLMYDCCSGSGCTVGRG 27
II III I : IIII:III III
Db 41 CKRGASCRRTSYDCTGSCNR--GRC 65

RESULT 9

Q9N628 PRELIMINARY; PRT; 66 AA.
AC Q9N628;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin precursor (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
[1]

RN SEQUENCE FROM N.A.
RC STRAIN=CCATH_III_9, AND CCATH_III_5;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-eating Conus";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174229; AAF89893.1; -.
DR EMBL; AF174226; AAF89890.1; -.
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7057 MW; E7AA5E310968B7DA CRC64;

Query Match 59.5%; Score 94; DB 5; Length 66;
Best Local Similarity 59.3%; Pred. No. 1.1e-06;
Matches 16; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 CKSKGAKSKLMYDCCSGSGCTVGRG 27
III III I : IIII:III III
Db 41 CKSTGASCRRTSYDCTGSCRS--GRC 65

RESULT 10

Q9N625 PRELIMINARY; PRT; 66 AA.
AC Q9N625;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin precursor (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.

```
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
   eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174228; AAF89892.1; -
DR EMBL; AF174221; AAF89885.1; -
DR EMBL; AF174222; AAF89886.1; -
DR EMBL; AF174224; AAF89888.1; -
DR EMBL; AF174225; AAF89889.1; -
DR HSSP; P05484; IMVI.
DR InterPro: IPR004214; Conotoxin.
DR pfam: PF02950; Conotoxin; 1
FT NON_TER 1
SQ SEQUENCE 66 AA; 7056 MW; EAL1338A6968B7DA CRC64;

Query Match 59.5%; Score 94; DB 5; Length 66;
Best Local Similarity 59.3%; Pred. No. 1.1e-06;
Matches 16; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

Db 1 CKSGAKGKSLMYDCSGSGCTGRC 27
    ||| ||| : ||||| |||
    41 CKSTGASCRRTSYDCCGTGSCRS--GRC 65

RESULT 11
Q9NCW2 PRELIMINARY; PRT; 66 AA.
ID Q9NCW2;
AC Q9NCW2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_III_3;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
   eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174223; AAF89887.1; -
DR HSSP; P05484; IMVI.
DR InterPro: IPR004214; Conotoxin.
DR pfam: PF02950; Conotoxin; 1
FT NON_TER 1
SQ SEQUENCE 66 AA; 7026 MW; EAL1339E382DB7DA CRC64;

Query Match 59.5%; Score 94; DB 5; Length 66;
Best Local Similarity 59.3%; Pred. No. 1.1e-06;
Matches 16; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

Qy 1 CKSGAKGKSLMYDCSGSGCTGRC 27
    ||| ||| : ||||| |||
    41 CKSTGASCRRTSYDCCGTGSCRS--GRC 65

Db 1 CKSGAKGKSLMYDCSGSGCTGRC 27
    ||| ||| : ||||| |||
    41 CKSTGASCRRTSYDCCGTGSCRS--GRC 65

RESULT 12
Q9NCW1 PRELIMINARY; PRT; 66 AA.
ID Q9NCW1;
AC Q9NCW1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
```

```
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_III_7;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
   eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174227; AAF89891.1; -
DR HSSP; P05484; IMVI.
DR InterPro: IPR004214; Conotoxin.
DR pfam: PF02950; Conotoxin; 1
FT NON_TER 1
SQ SEQUENCE 66 AA; 7066 MW; EAL1338A6968B415 CRC64;

Query Match 58.9%; Score 93; DB 5; Length 66;
Best Local Similarity 59.3%; Pred. No. 1.5e-06;
Matches 16; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

Qy 1 CKSGAKGKSLMYDCSGSGCTGRC 27
    ||| ||| : ||||| |||
    41 CKSTGASCRRTPYDCCGTGSCRS--GRC 65

Db 1 CKSGAKGKSLMYDCSGSGCTGRC 27
    ||| ||| : ||||| |||
    41 CKSTGASCRRTPYDCCGTGSCRS--GRC 65

RESULT 13
Q9NCV6 PRELIMINARY; PRT; 66 AA.
ID Q9NCV6;
AC Q9NCV6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_R_3;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
   eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174237; AAF89901.1; -
DR HSSP; P05484; IMVI.
DR InterPro: IPR004214; Conotoxin.
DR pfam: PF02950; Conotoxin; 1
FT NON_TER 1
SQ SEQUENCE 66 AA; 7084 MW; EAL1338A68C617DA CRC64;

Query Match 58.9%; Score 93; DB 5; Length 66;
Best Local Similarity 59.3%; Pred. No. 1.5e-06;
Matches 16; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

Qy 1 CKSGAKGKSLMYDCSGSGCTGRC 27
    ||| ||| : ||||| |||
    41 CKSTGASCRRTSYDCCGTGSCDR--GRC 65

Db 1 CKSGAKGKSLMYDCSGSGCTGRC 27
    ||| ||| : ||||| |||
    41 CKSTGASCRRTSYDCCGTGSCDR--GRC 65

RESULT 14
Q9NCV7 PRELIMINARY; PRT; 66 AA.
ID Q9NCV7;
AC Q9NCV7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_R.2;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
eating Conus."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174236; AAF89900.1; -;
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1 1
SQ SEQUENCE 66 AA; 7053 MW; 7453798A6968B31B CRC64;

Query Match 58.2%; Score 92; DB 5; Length 66;
Best Local Similarity 55.6%; Pred. No. 2.1e-06;
Matches 15; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 1 CKSGKAKCSKLMYDCCSGSGTGVRC 27
I: :||| | | ||||:|||| |||
Db 41 CQGRGASCRRTSYDCTGSCRS--GRC 65

RESULT 15

Q9NCW4 PRELIMINARY; PRT; 66 AA.
AC Q9NCW4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_11_5;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
eating Conus."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174218; AAF89882.1; -;
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1 1
SQ SEQUENCE 66 AA; 6995 MW; E445338A6AA7A1AC CRC64;

Query Match 56.3%; Score 89; DB 5; Length 66;
Best Local Similarity 55.6%; Pred. No. 5.8e-06;
Matches 15; Conservative 2; Mismatches 8; Indels 2; Gaps 1;

QY 1 CKSGKAKCSKLMYDCCSGSGTGVRC 27
I: ||| | | : | |||| |||
Db 41 CKRGASCRRTSYGCTGSCRS--GRC 65

Search completed: February 26, 2003, 08:39:46
Job time : 96.1538 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:31:34 ; Search time 13.1538 Seconds
(without alignments)
85.136 Million cell updates/sec

Title: US-09-673-490B-5

Perfect score: 158

Sequence: 1 CKSGAKGCKLMYDCCSGSGTGVRG 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	158	100.0	73	1 CXOD_CONCT	P58920 conus catus
2	121	76.6	27	1 CX07_CONCN	P58916 conus conso
3	114	72.2	71	1 CX0A_CONMA	P05484 conus magus
4	109.5	69.3	26	1 CXOC_CONCT	P58919 conus catus
5	107.5	68.0	29	1 CXOC_CONMA	P37300 conus magus
6	103	65.2	25	1 CX0B_CONCT	P58918 conus catus
7	96.5	61.1	72	1 CX0B_CONST	P28881 conus stria
8	96	60.8	29	1 CX0A_CONMA	Q26350 conus magus
9	94	59.5	71	1 CX0A_CONCT	P58917 conus catus
10	93	58.9	25	1 CX0B_CONMA	P05485 conus magus
11	85	53.8	71	1 CX03_CONST	Q9x2k2 conus stria
12	71.5	45.3	52	1 CTL2_NPVOP	O10286 orgyia pseu
13	70.5	44.6	73	1 CX06_CONGE	P01522 conus geogr
14	64.5	40.8	29	1 CX07_CONGE	P05483 conus geogr
15	62.5	39.6	37	1 TXP3_APTSC	P49268 aptostichus
16	59.5	37.7	61	1 TXF1_HORSE	P02800 equus caball
17	59.5	37.7	66	1 MT3_RAT	P37361 rattus norv
18	59.5	37.7	68	1 MT3_MOUSE	P28184 mus musculu
19	58.5	37.0	26	1 CX06_CONTU	P58915 conus tulip
20	58.5	37.0	325	1 Y856_TREPA	O83828 treponema p
21	58	36.7	27	1 CX0B_CONTE	P24159 conus texti
22	58	36.7	78	1 CXDA_CONTE	P18511 conus texti
23	57.5	36.4	27	1 CX06_CONRA	P58914 conus radia
24	57	36.1	26	1 CX07_CONTE	P56714 conus texti
25	57	36.1	61	1 MT1L_HUMAN	P80297 homo sapien
26	56.5	35.8	63	1 MT2_COLL1	P15787 columba liv
27	56.5	35.8	68	1 MT3_HORSE	P37360 equus caball
28	56.5	35.8	68	1 MT3_HUMAN	P25713 homo sapien
29	56.5	35.8	68	1 MT3_PIG	P55944 sus scrofa
30	56	35.4	72	1 MT13_MYTED	P80248 mytilus edu
31	55	34.8	60	1 MT_OREMO	P52726 oreochromis
32	55	34.8	61	1 MT2E_RABIT	P80292 oryctolagus
33	54.5	34.5	53	1 CTL1_NPVOP	O10367 orgyia pseu

34	54.5	34.5	61	1	MT2B_PIG	P79380 sus scrofa
35	54.5	34.5	63	1	MT1_COLL1	P15786 columba liv
36	54	34.2	27	1	MT2_COLL1	Q00369 colletoiric
37	54	34.2	37	1	TXOF_HADVE	P81399 hadronyche
38	54	34.2	68	1	MT_LYTPI	O02033 lytechinus
39	54	34.2	494	1	AMVR_DROPS	O18552 drosophila
40	54	34.2	556	1	OM6_CHLPN	P23700 chlamydia p
41	53.5	33.9	61	1	MT1A_HUMAN	P04731 homo sapien
42	53.5	33.9	72	1	MT14_MYTED	P80249 mytilus edu
43	53	33.5	61	1	MT2A_PIG	P79379 sus scrofa
44	53	33.5	61	1	MT2_BOVIN	P09579 bos taurus
45	52.5	33.2	43	1	MTB_COLLVI	P27087 colinus vir

ALIGNMENTS

RESULT 1
CXOD_CONCT STANDARD; PRT; 73 AA.
AC P58920;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Omega-conotoxin CVID precursor.
OS Conus catus (Cat cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_Taxid=101291;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 46-72, SYNTHESIS, AND STRUCTURE BY NMR.
RC TISSUE=Venom duct, and Venom;
RX PubMed=10938268;
RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A., Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A., Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
RA "Novel omega-conotoxins from Conus catus discriminate among neuronal calcium channel subtypes";
RT J. Biol. Chem. 275:35335-35344(2000).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC) (By similarity). This toxin blocks N-type calcium channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE FAMILY.
KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor; Amidation; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 45
FT PEPTIDE 46 72 OMEGA-CONOTOXIN CVID.
FT DISULFID 46 61 BY SIMILARITY.
FT DISULFID 53 65 BY SIMILARITY.
FT DISULFID 60 72 BY SIMILARITY.
FT MOD_RES 72 72 AMIDATION (G-73 PROVIDE AMIDE GROUP).
SQ SEQUENCE 73 AA; 7748 MW; CACEBD30C77DAEC3 CRC64;
Query Match 100.0%; Score 158; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CKSGAKGCKLMYDCCSGSGTGVRG 27
|||||
Db 46 CKSGAKGCKLMYDCCSGSGTGVRG 72
RESULT 2
CX07_CONCN STANDARD; PRT; 27 AA.
AC P58916;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Omega-conotoxin CNV11A.
 OS Conus consors (Slinged cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=101297;
 RN [1]
 RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX PubMed=11724570;
 RA Favreau P., Gilles N., Lamthanh H., Bournaud R., Shimahara T.,
 RA Bouet F., Laboute P., Letourneux Y., Menez A., Molgo J., Le Gall F.;
 RT "A new omega-conotoxin that targets N-type voltage-sensitive calcium
 RL channels with unusual specificity.";
 RL Biochemistry 40:14567-14575(2001).
 CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC). This toxin
 CC blocks N-type calcium channels, but unexpectedly, does not show
 CC any blocking activity at amphibian neuromuscular junction. Causes
 CC shaking activity, and, at higher doses, causes mild tremors when
 CC injected intracerebroventricularly into mice. Causes paralysis,
 CC and, at higher doses, causes death when injected intramuscularly
 CC into fish.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=2847.74; METHOD=Electrospray.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 CC FAMILY.
 KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
 KW Hydroxylation; Amidation.
 FT BINDING 13 13 ESSENTIAL FOR CALCIUM CHANNEL BINDING (BY
 FT SIMILARITY).
 FT DISULFD 1 16 BY SIMILARITY.
 FT DISULFD 8 20 BY SIMILARITY.
 FT DISULFD 15 27 BY SIMILARITY.
 FT MOD_RES 7 7 HYDROXYLATION.
 FT MOD_RES 27 27 AMIDATION.
 SQ SEQUENCE 27 AA: 2839 MW: 89DEFD1491F2CB4A CRC64;
 Query Match 76.68; Score 121; DB 1; Length 27;
 Best Local Similarity 70.48; Pred. No. 5.8e-09;
 Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CKSGKAKSKLMYDCSCSGSGTVCRC 27
 Db 1 CKRGAPCTRLMYDCCHSCSCSSRGRC 27
 RESULT 3
 ID CXOA_CONMA STANDARD; * PRT; 71 AA.
 P05484:
 01-NOV-1988 (Rel. 09, Created)
 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Omega-conotoxin MVIIA precursor (SNX-111) (Ziconotide).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6492;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Venom duct;
 RX PubMed=10938268;
 RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
 RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
 RA Matheson J.E.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
 RT "Novel omega-conotoxins from Conus catus discriminate among neuronal
 RL calcium channel subtypes.";
 RL J. Biol. Chem. 275:35335-35344(2000).
 RN [2]
 RN SEQUENCE OF 46-70.
 RX MEDLINE=86070213; PubMed=4071055;
 RA Olivera B.M., Gray W.R., Zeikus R.D., McIntosh J.M., Varga J.,
 RA Rivier J.E., de Santos V., Cruz L.J.;
 RT "Peptide neurotoxins from fish-hunting cone snails.";
 RL Science 230:1338-1343(1985).
 RN [3]
 RN SEQUENCE OF 46-70.
 RX MEDLINE=87299637; PubMed=2441741;
 RA Olivera B.M., Cruz L.J., de Santos V., Lecheminant G.W., Griffin D.,
 RA Zeikus R.D., McIntosh J.M., Galyean R., Varga J., Gray W.R.,
 RA Rivier J.E.;
 RT "Neuronal calcium channel antagonists. Discrimination between calcium
 RL channel subtypes using omega-conotoxin from Conus magus venom.";
 RL Biochemistry 26:2086-2090(1987).
 RN [4]
 RN DISULFIDE BONDS.
 RX PubMed=8537186;
 RA Chung D., Gaur S., Bell J.R., Ramachandran J., Nadasdi L.;
 RT "Determination of disulfide bridge pattern in omega-conopeptides.";
 RL Int. J. Pept. Protein Res. 46:320-325(1995).
 RN [5]
 RN SYNTHESIS, AND MUTAGENESIS OF LYS-47 AND TYR-58.
 RX PubMed=7826361;
 RA Kim J.I., Takahashi M., Ohtake A., Wakamiya A., Sato K.;
 RT "Tyrl3 is essential for the activity of omega-conotoxin MVIIA and
 RL GVIA, specific N-type calcium channel blockers.";
 RL Biochem. Biophys. Res. Commun. 206:449-454(1995).
 RN [6]
 RN STRUCTURE BY NMR.
 RX MEDLINE=95367553; PubMed=7640281;
 RA Kohno T., Kim J.-I., Kobayashi K., Kodera Y., Maeda T., Sato K.;
 RT "Three-dimensional structure in solution of the calcium channel
 RL blocker omega-conotoxin MVIIA.";
 RL Biochemistry 34:10256-10265(1995).
 RN [7]
 RN STRUCTURE BY NMR.
 RX PubMed=7656969;
 RA Basus V.J., Nadasdi L., Ramachandran J., Miljanich G.P.;
 RT "Solution structure of omega-conotoxin MVIIA using 2D NMR
 RL spectroscopy.";
 RL FEBS Lett. 370:163-169(1995).
 RN [8]
 RN STRUCTURE BY NMR.
 RX MEDLINE=97070382; PubMed=8913308;
 RA Nielsen K.J., Thomas L., Lewis R.J., Alewood P.F., Craik D.J.;
 RT "A consensus structure for omega-conotoxins with different
 RL selectivities for voltage-sensitive calcium channel subtypes:
 RT comparison of MVIIA, SVIB and SNX-202.";
 RL J. Mol. Biol. 263:297-310(1996).
 RN [9]
 RN STRUCTURE BY NMR.
 RX PubMed=10373375;
 RA Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
 RA Lewis R.J.;
 RT "Structure-activity relationships of omega-conotoxins MVIIA, MWIIC and
 RL 14 loop splice hybrids at N and P/Q-type calcium channels.";
 RL J. Mol. Biol. 289:1405-1421(1999).
 RN [10]
 RN STRUCTURE BY NMR.
 RX PubMed=10747778;
 RA Atkinson R.A., Kieffer B., Dejaegere A., Sirockin F., Lefevre J.-F.;
 RT "Structural and dynamic characterization of omega-conotoxin MVIIA: the
 RL binding loop exhibits slow conformational exchange.";
 RL Biochemistry 39:3908-3919(2000).
 RN [11]
 RN STRUCTURE BY NMR.
 RX MEDLINE=21243158; PubMed=11344322;
 RA Goldenberg D.P., Koehn R.E., Gilbert D.E., Wagner G.;
 RT "Solution structure and backbone dynamics of an omega-conotoxin
 RL precursor.";
 RL Protein Sci. 10:538-550(2001).
 CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC). This toxin
 CC blocks N-type calcium channels.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- PHARMACEUTICAL: Is under clinical trial by Neurx. It blocks acute
 CC pain in patients who no longer obtain relief from opiate drugs. It
 CC is 100 to 1000 times more potent than morphine. By blocking
 CC calcium channels it disable nerves that transmit pain signals.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 CC FAMILY.
 CC -!- DATABASE: NAME=Ziconotide Source; NOTE=Web site on ziconotide;
 CC WWW="http://docmd.com/ziconotide/".
 CC PIR: C50133; C60133.
 CC DR: JH0700; JH0700.
 CC DR: PDB: 1OMG; 03-APR-96.
 CC DR: PDB: 1MWI; 12-AUG-97.
 CC DR: PDB: 1DW4; 01-MAR-00.
 CC DR: PDB: 1DW5; 01-MAR-00.
 CC DR: PDB: 1PEO; 23-AUG-00.
 CC KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
 KW Amidation; Signal; 3D-structure; Pharmaceutical.
 CC SIGNAL 1 22
 CC FT PROPEP 23 45
 CC FT PEPTIDE 46 70
 CC FT DISULFID 46 61
 CC FT DISULFID 53 65
 CC FT DISULFID 60 70
 CC FT MOD_RES 70 70
 CC FT MUTAGEN 47 47
 CC FT MUTAGEN 58 58
 CC SQ SEQUENCE 71 AA; 7587 MW; E2A32725C81AF3D CRC64;
 Query Match 72.2%; Score 114; DB 1; Length 71;
 Best Local Similarity 70.4%; Pred. No. 8.7e-08;
 Matches 19; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
 QY 1 CKSGKAKSKLMYDCSGSGSGTVGRC 27
 DB 46 CKRGKAKSKRLMYDCTGSCRS--GRC 70
 RESULT 4
 CXOC_CONCT STANDARD; PRT; 26 AA.
 AC P58919;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Omega-conotoxin CVIC.
 OS Conus catus (Cat cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 CC NCBI_TaxID=101291;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=venom;
 RX PubMed=10938268;
 RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
 RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
 RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
 FT "Novel omega-conotoxins from Conus catus discriminate among neuronal
 CC calcium channel subtypes.";
 CC J. Biol. Chem. 275:35335-35344 (2000).
 CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC) (By
 CC similarity). This toxin blocks N-, P-, and Q-type calcium
 CC channels.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 CC FAMILY.
 CC KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
 KW Amidation.
 CC DISULFID 1 16 BY SIMILARITY.
 CC FT DISULFID 8 20 BY SIMILARITY.

FT DISULFID 15 26 BY SIMILARITY.
 FT MOD_RES 26 26 AMIDATION.
 SQ SEQUENCE 26 AA; 2790 MW; 56EFC382335C4A8B CRC64;
 Query Match 69.3%; Score 109.5; DB 1; Length 26;
 Best Local Similarity 70.4%; Pred. No. 1.4e-07;
 Matches 19; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
 QY 1 CKSGKAKSKLMYDCSGSGSGTVGRC 27
 DB 1 CKRGKAKSKLMYDCSGSGTVGRC 26
 RESULT 5
 CXOC_CONWA STANDARD; PRT; 29 AA.
 ID CXOC_CONWA
 AC P37300;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Omega-conotoxin MVIIC precursor (SNX-230) (Fragment).
 OS Conus magus (Magus cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 CC NCBI_TaxID=6492;
 RN [1]
 RP SEQUENCE FROM N.A., AND SYNTHESIS.
 RX MEDLINE=92337922; PubMed=1352986;
 RA Hilliard D.R., Monje V.D., Mintz I.M., Bean B.P., Nadasdi L.,
 RA Ramachandran J., Miljanich G.P., Azimi-Zoonooz A., McIntosh J.M.,
 RA Cruz L.J., Imperial J.S., Olivera B.M.;
 RT "A new Conus peptide ligand for mammalian presynaptic Ca2+ channels.";
 RL Neuron 9:69-77(1992).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95248539; PubMed=7731037;
 RA Farr-Jones S., Miljanich G.P., Nadasdi L., Ramachandran J.,
 RA Basus V.J.;
 RT "Solution structure of omega-conotoxin MVIIC, a high affinity ligand
 RT of P-type calcium channels, using 1H NMR spectroscopy and complete
 RT relaxation matrix analysis.";
 RL J. Mol. Biol. 248:106-124(1995).
 RN [3]
 RP STRUCTURE BY NMR.
 RX PubMed=10373375;
 RA Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
 RA Lewis R.J.;
 RT "Structure-activity relationships of omega-conotoxins MVIIC and
 RT 14 loop splice hybrids at N and P/Q-type calcium channels.";
 RL J. Mol. Biol. 289:1405-1421(1999).
 RN [4]
 RP MUTAGENESIS OF TYR-15.
 RX PubMed=7677735;
 RA Kim J.I., Takahashi M., Martin-Moutot N., Seagar M.J., Ohtake A.,
 RA Sato K.;
 RT "Tyr13 is essential for the binding of omega-conotoxin MVIIC to the
 RT P/Q-type calcium channel.";
 RL Biochem. Biophys. Res. Commun. 214:305-309(1995).
 CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC). This toxin
 CC blocks N-type calcium channels as well as types of high-threshold
 CC voltage-gated calcium channels resistant to both dihydropyridines
 CC and omega-conotoxin GVIA.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 CC FAMILY.
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QY-1 CKSGAKCSKLMYDCCSGSGTGVRC 27

! FUNCTION: Omega COM and block voltage-s

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE FAMILY.
DR PIR: B34115; B34115.
DR PIR: JH0701; JH0701.
DR HSSP: P05484; IMVI.
KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
KW Amidation.
FT SIGNAL 1 16
FT DISULFID 8 20
FT DISULFID 15 25
FT MOD_RES 25 25
FT SEQUENCE 25 AA: 2626 MW: 4490
Query Match 58.9%; Score 93; DB 1; Length 25;
Best Local Similarity 55.6%; Pred. No. 1.4e-05;
Matches 15; Conservative 4; Mismatches 6; Indels 2; Gaps 1;
Qy 1 CKSGAKSKLMYDCSCSGCTVGRC 27
| | | | : | | | | | : | |
Db 1 CKGASCHRTSYDCCTGSCNR--GKC 25
| | | | : | | | | | : | |
RESULT 11
CXO3_CONST STANDARD; PRT; 71 AA.
ID CXO3_CONST
AC O9XK2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Omega-type conotoxin SO3 precursor.
GN SO3.
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Venom duct;
RC MEDLINE=20037955; PubMed=10573284;
RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
RT "Conopeptides from Conus striatus and Conus textile by cDNA
cloning.";
RL Peptides 20:1139-1144(1999).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
and block voltage-sensitive calcium channels (VSCC) (By
similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE FAMILY.

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EMBL: AF146348; AAD31908.1; -.
DR HSSP: P05484; IMVI.
DR InterPro: IPR004214; Conotoxin.
DR Pfam: PF02950; Conotoxin.
KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
KW Signal; Amidation.
FT SIGNAL 1 22
FT PROPEP 23 44
FT PEPTIDE 45 70
FT DISULFID 46 61
FT DISULFID 53 65
FT DISULFID 60 70
POTENTIAL.
OMEGA-TYPE CONOTOXIN SO3.
BY SIMILARITY.
BY SIMILARITY.

FT MOD_RES 70 70
FT SEQUENCE 71 AA: 7628 MW: 7628
AMIDATION (G-71 PROVIDE AMIDE GROUP) (POTENTIAL).
CE7070DCE3094D73 CRC64;
Query Match 53.8%; Score 85; DB 1; Length 71;
Best Local Similarity 48.1%; Pred. No. 0.0003;
Matches 13; Conservative 6; Mismatches 6; Indels 2; Gaps 1;
Qy 1 CKSGAKSKLMYDCSCSGCTVGRC 27
| | | | : | | | | | : | |
Db 46 CRAAGKPCSRITAYNCTGSCRS--GKC 70
| | | | : | | | | | : | |
RESULT 12
CTL2_NPVOP STANDARD; PRT; 52 AA.
ID CTL2_NPVOP
AC O10286;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Conotoxin-like peptide 2 precursor.
GN CTL-2.
OS Orygia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=164623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97271300; PubMed=9126251;
RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
RA Rohrmann G.F.;
RT "The sequence of the Orygia pseudotsugata multinucleocapsid nuclear
polyhedrosis virus genome.";
RL Virology 229:381-399(1997).
CC -!- SUBCELLULAR LOCATION: Secreted
CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE FAMILY.

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EMBL: U75930; AAC59029.1; -.
DR Signal.
KW SIGNAL 1 18
FT CHAIN 19 52
FT DISULFID 24 38
FT DISULFID 31 42
FT DISULFID 37 49
FT SEQUENCE 52 AA: 5604 MW: 5604
CONOTOXIN-LIKE PEPTIDE 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
Query Match 45.3%; Score 71.5; DB 1; Length 52;
Best Local Similarity 44.4%; Pred. No. 0.011;
Matches 12; Conservative 3; Mismatches 11; Indels 1; Gaps 1;
Qy 1 CKSGAKSKLMYDCSCSGCTVGRC 27
| | | | : | | | | | : | |
Db 24 CTETGRNC-QYSECCGACSAAGFC 49
| | | | : | | | | | : | |
RESULT 13
CXO6_CONGE STANDARD; PRT; 73 AA.
ID CXO6_CONGE
AC P01522;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Omega-conotoxin GVIA precursor (Shaker peptide) (SNX-124) [Contains:
Omega-conotoxin GVIB; Omega-conotoxin GVIC].

OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93069266; PubMed=1440648;
 RA Colledge C.J., Hunsperger J.P., Imperial J.S., Hillyard D.R.;
 RT "precursor structure of omega-conotoxin GVIA determined from a cDNA
 clone";
 RL Toxicon 30:1111-1116(1992).
 RN [2]
 RP SEQUENCE OF 46-73.
 RX MEDLINE=85072796; PubMed=6509012;
 RA Olivera B.M., McIntosh J.M., Cruz L.J., Luque F.A., Gray W.R.;
 RT "Purification and sequence of a presynaptic peptide toxin from Conus
 geographus venom";
 RL Biochemistry 23:5087-5090(1984).
 RN [3]
 RP STRUCTURE BY NMR OF GVIA.
 RX MEDLINE=94047089; PubMed=8230223;
 RA Pallaghy P.K., Duggan B.M., Pennington M.W., Norton R.S.;
 RT "Three-dimensional structure in solution of the calcium channel
 blocker omega-conotoxin";
 RL J. Mol. Biol. 234:405-420(1993).
 RN [4]
 RP STRUCTURE BY NMR OF GVIA.
 RX MEDLINE=93332945; PubMed=8338837;
 RA Davis J.H., Bradley E.K., Miljanich G.P., Nadasdi L.,
 Ramachandran J., Basus V.J.;
 RT "Solution structure of omega-conotoxin GVIA using 2-D NMR
 spectroscopy and relaxation matrix analysis";
 RL Biochemistry 32:7396-7405(1993).
 RN [5]
 RP STRUCTURE BY NMR OF GVIA.
 RX MEDLINE=99248506; PubMed=10231724;
 RA Pallaghy P.K., Norton R.S.;
 RT "Refined solution structure of omega-conotoxin GVIA: Implications for
 calcium channel binding";
 RL J. Pept. Res. 53:343-351(1999).
 CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 and block voltage-sensitive calcium channels (VSCC).
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 FAMILY.
 CC -----
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 CC -----
 DR EMBL; M84612; AAA81590.1; -
 DR PIR; A60133; NTKN6G.
 DR PIR; A44006; A44006.
 DR PDB; 2CCO; 15-JUL-98.
 DR PDB; 1OMC; 31-JAN-94.
 DR InterPro; IPR004214; Conotoxin.
 DR Pfam; PF02950; Conotoxin; 1.
 KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
 KW Hydroxylation; Amidation; Signal; 3D-structure.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 45
 FT PEPTIDE 46 73 OMEGA-CONOTOXIN GVIB.
 FT PEPTIDE 46 72 OMEGA-CONOTOXIN GVIA.
 FT PEPTIDE 46 71 OMEGA-CONOTOXIN GVIC.
 FT MOD_RES 49 49 HYDROXYLATION.
 FT MOD_RES 55 55
 FT MOD_RES 66 66 HYDROXYLATION.
 FT MOD_RES 72 72 AMIDATION (G-73 PROVIDE AMIDE GROUP) (IN

FT DISULFID 46 61 GVIA).
 FT DISULFID 53 64
 FT DISULFID 60 71
 FT STRAND 47 47
 FT TURN 49 50
 FT STRAND 52 52
 FT TURN 55 58
 FT STRAND 60 60
 FT STRAND 64 65
 FT TURN 66 69
 FT STRAND 70 71
 SQ SEQUENCE 73 AA; 7851 MW; 51A8C8FA630F7175 CRC64;
 Query Match 44.6%; Score 70.5; DB 1; Length 73;
 Best Local Similarity 48.1%; Pred. No. 0.018;
 Matches 13; Conservative 3; Mismatches 10; Indels 1; Gaps 1;
 QY 1 CKSKGAKCKLMYDCSCSGSGTVGRC 27
 III I: II I:II II:
 Db 46 CKSPGSCSPTSYNCCR-SCNPYTKRC 71
 RESULT 14
 CXO7_CONGE STANDARD; PRT; 29 AA.
 ID CXO7_CONGE STANDARD; PRT; 29 AA.
 AC P05483;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Omega-conotoxins GVIIA/GVIB (SNX-178).
 OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN [1]
 RP MEDLINE=86070213; PubMed=4071055;
 RA Olivera B.M., Gray W.R., Zeikus R.D., McIntosh J.M., Varga J.,
 Rivier J.E., de Santos V., Cruz L.J.;
 RT "Peptide neurotoxins from fish-hunting cone snails";
 RL Science 230:1338-1343(1985).
 CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 and block voltage-sensitive calcium channels (VSCC).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF CONOTOXIN GVIIA.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 CC FAMILY.
 DR PIR; A43620; A43620.
 DR PIR; B43620; B43620.
 KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
 KW Hydroxylation.
 FT MOD_RES 4 4 HYDROXYLATION.
 FT MOD_RES 7 7 HYDROXYLATION.
 FT DISULFID 1 16
 FT DISULFID 8 19
 FT DISULFID 15 26
 FT VARIANT 21 21 L->S (IN GVIIIB).
 SQ SEQUENCE 29 AA; 3290 MW; 57307C69583FB1E7 CRC64;
 Query Match 40.8%; Score 64.5; DB 1; Length 29;
 Best Local Similarity 48.1%; Pred. No. 0.048;
 Matches 13; Conservative 3; Mismatches 10; Indels 1; Gaps 1;
 QY 1 CKSKGAKCKLMYDCSCSGSGTVGRC 27
 III I: II I:II II:
 Db 1 CKSPGTPCSRGMRDCT-SCLLYSNKC 26
 RESULT 15
 TXP3_APTSC STANDARD; PRT; 37 AA.
 ID TXP3_APTSC STANDARD; PRT; 37 AA.

P49268;
AC 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aptotoxin III (Paralytic peptide III) (PP III).
OS Aptostichus schlingeri (Trap-door spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Mygalomorphae; Cyrtauchenidae; Aptostichus.
OX NCBI_TaxID=12944;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=93069259; PubMed=1440641;
RA Skinner W.S., Dennis P.A., Li J.P., Quistad G.B.;
RT "Identification of insecticidal peptides from venom of the trap-door
spider, Aptostichus schlingeri (Ctenizidae).";
RL Toxicon 30:1043-1050(1992).
CC -!- FUNCTION: IS BOTH PARALYTIC AND LETHAL, WHEN INJECTED INTO
CC LEPIDOPTERAN LARVAE. IS A SLOWER ACTING TOXIN, BEING LETHAL AT 24
CC HR, BUT NOT PARALYTIC AT 1 HR POST-INJECTION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- PTM: FOUR DISULFIDE BONDS ARE PRESENT.
CC -!- MISCELLANEOUS: LD(50) IS 0.50 MG/KG BY SUBCUTANEOUS INJECTION.
CC -!- SIMILARITY: TO APTOTOXIN VII.
KW Toxin; Neurotoxin.
SQ SEQUENCE 37 AA; 3769 MW; CBD01091694E1908 CRC64;
Query Match 39.6%; Score 62.5; DB 1; Length 37;
Best Local Similarity 40.7%; Pred. No. 0.1;
Matches 11; Conservative 3; Mismatches 12; Indels 1; Gaps 1;
QY 1 CKSKGAKGCKLMYDCSGSCSGTGVGR 27
| | | | : | | | : | |
Db 1 CNSKGTPTCN-ADECCGGKCAYNVWNC 26

Search completed: February 26, 2003, 08:37:20
Job time : 14.1538 secs

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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:39:54 ; Search time 3.84615 Seconds
(without alignments)
58.846 Million cell updates/sec

Title: US-09-673-490B-1
Perfect score: 30
Sequence: 1 SGTGVR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174566 seqs, 37721826 residues
Total number of hits satisfying chosen parameters: 174566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	96.7	385	9	US-10-260-877-106
2	27	90.0	95	9	US-09-941-831-27
3	27	90.0	150	10	US-09-781-867-4
4	27	90.0	260	12	US-10-051-986-4
5	27	90.0	417	10	US-09-781-867-2
6	27	90.0	472	10	US-09-730-989-2
7	27	90.0	1300	10	US-09-815-242-4903
8	27	90.0	1300	10	US-09-815-242-10906
9	26	86.7	49	9	US-10-016-157A-238
10	26	86.7	60	10	US-09-764-864-1187
11	26	86.7	75	9	US-09-738-626-3846
12	26	86.7	105	9	US-10-108-605-313
13	26	86.7	165	10	US-09-764-864-1528
14	26	86.7	171	9	US-09-738-626-6387
15	26	86.7	252	10	US-09-764-864-1108
16	26	86.7	255	10	US-09-927-738-5
17	26	86.7	271	9	US-09-738-626-6380
18	26	86.7	308	9	US-09-860-670-111
19	26	86.7	308	10	US-09-764-870-376

20 26 86.7 354 9 US-09-978-295A-178 Sequence 178, App
21 26 86.7 354 9 US-09-978-697-178 Sequence 178, App
22 26 86.7 354 9 US-09-978-192A-178 Sequence 178, App
23 26 86.7 354 9 US-09-999-832A-178 Sequence 178, App
24 26 86.7 354 9 US-09-978-189-178 Sequence 178, App
25 26 86.7 354 9 US-10-028-072-400 Sequence 400, App
26 26 86.7 354 9 US-10-121-049-400 Sequence 400, App
27 26 86.7 354 9 US-10-123-904-400 Sequence 400, App
28 26 86.7 354 9 US-10-140-470-400 Sequence 400, App
29 26 86.7 354 9 US-10-175-746-400 Sequence 400, App
30 26 86.7 354 9 US-10-176-918-400 Sequence 400, App
31 26 86.7 354 9 US-10-176-921-400 Sequence 400, App
32 26 86.7 354 9 US-10-137-865-400 Sequence 400, App
33 26 86.7 354 9 US-10-140-474-400 Sequence 400, App
34 26 86.7 354 9 US-10-142-431-400 Sequence 400, App
35 26 86.7 354 9 US-10-143-114-400 Sequence 400, App
36 26 86.7 372 10 US-09-818-066-64 Sequence 64, Appli
37 26 86.7 396 10 US-09-927-738-3 Sequence 3, Appli
38 26 86.7 457 9 US-09-712-363-198 Sequence 198, App
39 26 86.7 465 10 US-09-923-779-151 Sequence 151, App
40 26 86.7 473 10 US-09-925-297-567 Sequence 567, App
41 26 86.7 512 9 US-09-738-626-3817 Sequence 3817, Ap
42 26 86.7 568 9 US-09-738-626-3950 Sequence 3950, Ap
43 26 86.7 615 9 US-09-738-626-6018 Sequence 6018, Ap
44 26 86.7 619 10 US-09-855-750-2 Sequence 2, Appli
45 26 86.7 919 9 US-09-738-626-6970 Sequence 6970, Ap

ALIGNMENTS

RESULT 1

US-10-260-877-106

; Sequence 106, Application US/10260877

; Publication No. US20030021813A1

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Chovan, Linda E.

; APPLICANT: Hessler, Paul E.

; APPLICANT: Reich, Karl A.

; TITLE OF INVENTION: ESSENTIAL BACTERIA GENES AND GENOME

; TITLE OF INVENTION: SCANNING IN HAEMOPHILUS INFLUENZAE FOR THE IDENTIFICATION OF

; TITLE OF INVENTION: 'ESSENTIAL GENES'

; FILE REFERENCE: 6565.US.P1

; CURRENT APPLICATION NUMBER: US/10/260;877

; CURRENT FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: US/09/649,145

; PRIOR FILING DATE: 2000-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 106

; LENGTH: 385

; TYPE: PRT

; ORGANISM: H. influenzae

US-10-260-877-106

Query Match 96.7%; Score 29; DB 9; Length 385;

Best Local Similarity 83.3%; Pred. No. 1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTGVR 6

Db 268 SGTIGR 273

RESULT 2

US-09-941-831-27

; Sequence 27, Application US/09941831

; Patent No. US20020160493A1

; GENERAL INFORMATION:

; APPLICANT: Ebner et al.

; TITLE OF INVENTION: PT049P1

; FILE REFERENCE: Serine/Threonine Phosphatase Polynucleotides, Polypeptides, and An

; CURRENT APPLICATION NUMBER: US/09/941.831
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/06256
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/186,350
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-941-831-27

Query Match 90.08; Score 27; DB 9; Length 95;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
|||||
DB 4 SGTVGK 9

RESULT 3
S-09-781-867-4
; Sequence 4, Application US/09781867
; Patent No. US20020019029A1
; GENERAL INFORMATION:
; APPLICANT: BARNES, MICHAEL R.
; APPLICANT: TESTA, TANIA TAMSON
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30043-C1
; CURRENT APPLICATION NUMBER: US/09/781.867
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: EP 98300711.3
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: UK 9900883.1
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: 09/240,235
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 150
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (59)
US-09-781-867-4

Query Match 90.08; Score 27; DB 10; Length 150;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
|||||
DB 143 AGTVGR 148

RESULT 4
US-10-051-986-4
; Sequence 4, Application US/10051986
; Patent No. US20020146770A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Tang, Y. Tom
; Lal, Preeti
; Guegler, Karl J.
; Corley, Neil C.
; Patterson, Chandra
; Batra, Sajeev
; Baughn, Mariah R.

; TITLE OF INVENTION: RAS PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/051.986
; FILING DATE: 15-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,551
; FILING DATE: DECEMBER 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSTUT08
; CLONE: 1651593
; SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
US-10-051-986-4

Query Match 90.08; Score 27; DB 12; Length 260;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
|||||
DB 45 TGTVGR 50

RESULT 5
US-09-781-867-2
; Sequence 2, Application US/09781867
; Patent No. US20020019029A1
; GENERAL INFORMATION:
; APPLICANT: BARNES, MICHAEL R.
; APPLICANT: TESTA, TANIA TAMSON
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30043-C1
; CURRENT APPLICATION NUMBER: US/09/781.867
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: EP 98300711.3
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: UK 9900883.1
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: 09/240,235
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 417
; TYPE: PRT
; ORGANISM: HOMO SAPIENS

US-09-781-867-2

Query Match 90.0%; Score 27; DB 10; Length 417;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
:|||||
Db 355 AGTVGR 360

RESULT 6

US-09-730-989-2
; Sequence 2, Application US/09730989
; Patent No. US20020061552A1

GENERAL INFORMATION:

APPLICANT: Yan, Dong
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: MAMMALIAN DISHEVELLED-ASSOCIATED PROTEINS
FILE REFERENCE: PP-01657.002 / 200130.518
CURRENT APPLICATION NUMBER: US/09/730,989
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 29

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2
LENGTH: 472

TYPE: PRT

ORGANISM: Mus musculus

US-09-730-989-2

Query Match 90.0%; Score 27; DB 10; Length 472;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
:|||||
Db 56 ACTVGR 61

RESULT 7

US-09-815-242-4903
; Sequence 4903, Application US/09815242
; Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4903
LENGTH: 1300

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-815-242-4903

Query Match 90.0%; Score 27; DB 10; Length 1300;
Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
:|||||
Db 883 SGTGK 888

RESULT 8

US-09-815-242-10906
; Sequence 10906, Application US/09815242
; Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10906

LENGTH: 1300

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-815-242-10906

Query Match 90.0%; Score 27; DB 10; Length 1300;
Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
:|||||
Db 883 SGTGK 888

RESULT 9

US-10-016-157A-238
; Sequence 238, Application US/10016157A
; Publication No. US20020192220A1

GENERAL INFORMATION:

APPLICANT: Sun, Yongming

APPLICANT: Recipon, Herve

APPLICANT: Ghosh, Malavika

APPLICANT: Liu, Chenghua

```
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pro
; FILE REFERENCE: DEX-0253
; CURRENT APPLICATION NUMBER: US/10/016.157A
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,717
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 250
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-157A-238

Query Match      86.7%; Score 26; DB 9; Length 49;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTGVR 6
   :||:|
Db 40 AGTGR 45

RESULT 10
US-09-764-864-1187
; Sequence 1187, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1187
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1187

Query Match      86.7%; Score 26; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTVGR 6
   :|||
Db 13 GTVGR 17

RESULT 11
US-09-738-626-3846
; Sequence 3846, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
```

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; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3846
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3846

Query Match      86.7%; Score 26; DB 9; Length 75;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTGVR 6
   :||:|
Db 46 SGSVR 51

RESULT 12
US-10-108-605-313
; Sequence 313, Application US/10108605
; Patent No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCOD
; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
; FILE REFERENCE: 31133B
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/176,418
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 313
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-108-605-313

Query Match      86.7%; Score 26; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTVGR 6
   :|||
Db 73 GTVGR 77

RESULT 13
US-09-764-864-1528
; Sequence 1528, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1528
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1528

Query Match 86.7%; Score 26; DB 10; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTVGR 6
|||||
Db 117 GTVGR 121

RESULT 14

US-09-738-626-6387
; Sequence 6387, Application US/09738626
; Publication No. US20020197605A1

GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6387
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6387

Query Match 86.7%; Score 26; DB 9; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTVGR 6
|||||
Db 3 GTVGR 7

RESULT 15

US-09-764-864-1108
; Sequence 1108, Application US/09764864
; Patent No. US20020132753A1

GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1108

; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1108

Query Match 86.7%; Score 26; DB 10; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTVGR 6
|||||
Db 94 GTVGR 98

Search completed: February 26, 2003, 08:52:59
Job time : 3.84615 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:35:20 ; Search time 5.23077 Seconds
(without alignments)
33.750 Million cell updates/sec

Title: US-09-673-490B-1
Perfect score: 30
Sequence: 1 SGTVGR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	29	96.7	745	2	US-08-479-403-2
5	29	96.7	745	3	US-08-835-734-2
6	27	90.0	260	4	US-09-075-434-4
7	27	90.0	341	1	US-08-314-309A-19
8	27	90.0	425	4	US-09-134-001C-2895
9	27	90.0	524	3	US-08-557-210A-3
10	27	90.0	539	3	US-08-557-210A-4
11	27	90.0	539	3	US-08-557-210A-5
12	27	90.0	561	2	US-08-474-169-8
13	27	90.0	691	5	PCT-US91-08442-2
14	27	90.0	756	1	US-08-434-730-16
15	26	86.7	16	4	US-08-602-999A-190
16	26	86.7	16	4	US-09-500-124-190
17	26	86.7	27	3	US-09-053-197A-47
18	26	86.7	27	4	US-09-085-761A-52
19	26	86.7	65	3	US-08-750-141A-8
20	26	86.7	331	4	US-08-849-751-4
21	26	86.7	331	4	US-09-478-816-4
22	26	86.7	345	4	US-08-985-492-10
23	26	86.7	353	4	US-08-985-492-4
24	26	86.7	354	4	US-08-985-492-6
25	26	86.7	372	2	US-08-683-262B-64
26	26	86.7	372	4	US-09-361-707-64
27	26	86.7	422	1	US-08-132-649-4

28 26 86.7 422 3 US-08-767-579-4 Sequence 4, Appli
29 26 86.7 465 4 US-08-985-492-15 Sequence 15, Appli
30 26 86.7 500 4 US-08-985-492-8 Sequence 8, Appli
31 26 86.7 517 1 US-08-132-649-2 Sequence 2, Appli
32 26 86.7 517 1 US-08-764-343-4 Sequence 4, Appli
33 26 86.7 517 3 US-08-767-579-2 Sequence 2, Appli
34 26 86.7 661 1 US-08-232-538-12 Sequence 12, Appli
35 26 86.7 661 2 US-08-786-164-12 Sequence 12, Appli
36 26 86.7 687 1 US-08-232-538-6 Sequence 6, Appli
37 26 86.7 687 2 US-08-786-164-6 Sequence 6, Appli
38 26 86.7 687 4 US-09-427-353-2 Sequence 2, Appli
39 26 86.7 724 4 US-09-562-737-24 Sequence 24, Appli
40 26 86.7 758 2 US-08-222-617A-6 Sequence 6, Appli
41 26 86.7 758 2 US-08-874-678-1 Sequence 1, Appli
42 26 86.7 758 3 US-08-643-839-1 Sequence 1, Appli
43 26 86.7 758 4 US-09-051-363-24 Sequence 24, Appli
44 26 86.7 758 4 US-09-348-886-1 Sequence 1, Appli
45 26 86.7 780 1 US-08-232-538-14 Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-09-004-838-11
; Sequence 11, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Conferring Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-0788100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1402 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..1402
; OTHER INFORMATION: /note= "RLG1a amino acids"
US-09-004-838-11

Query Match 100.0%; Score 30; DB 4; Length 1402;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
| | | | |
DB 530 SGTVGR 535

RESULT 2
US-09-134-001C-4946
; Sequence 4946, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GPC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4946
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4946

Query Match 96.7%; Score 29; DB 4; Length 234;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
| | | | |
DB 9 SGTIGR 14

RESULT 3
US-08-136-277-2
; Sequence 2, Application US/08136277
; Patent No. 5644045
; GENERAL INFORMATION:
; APPLICANT: MANDEL, Jean-Louis
; APPLICANT: AUBOURG, Patrick
; APPLICANT: MOSSE, Jean
; APPLICANT: SARDE, Claude
; TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Young & Thompson
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,277
; FILING DATE: 15-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: B2272
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-136-277-2

Query Match 96.7%; Score 29; DB 1; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
| | | | |
DB 447 SGTIGR 452

RESULT 4
US-08-479-403-2
; Sequence 2, Application US/08479403
; Patent No. 5869039
; GENERAL INFORMATION:
; APPLICANT: MANDEL, Jean-Louis
; APPLICANT: AUBOURG, Patrick
; APPLICANT: MOSSE, Jean
; APPLICANT: SARDE, Claude
; TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Young & Thompson
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,403
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: B2272DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-403-2

Query Match 96.7%; Score 29; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
| | | | |
DB 447 SGTIGR 452


```
RESULT 5
US-08-835-734-2
; Sequence 2, Application US/08835734
; Patent No. 6013769
; GENERAL INFORMATION:
; APPLICANT: MANDEL, Jean-Louis
; APPLICANT: AUBOURG, Patrick
; APPLICANT: MOSSER, Jean
; APPLICANT: SARDE, Claude
; TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
; TITLE OF INVENTION: CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Young & Thompson
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,734
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/479,403
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: B272DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-835-734-2

Query Match 96.7%; Score 29; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
DB 447 SGTIGR 452

RESULT 6
US-09-075-454-4
; Sequence 4, Application US/09075454
; Patent No. 6391580
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Patterson, Chandra
; APPLICANT: Batra, Sajeev
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: RAS PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
```

```
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,454
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,551
FILING DATE: DECEMBER 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT08
CLONE: 1651593
US-09-075-454-4

Query Match 90.0%; Score 27; DB 4; Length 260;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
DB 45 TGTVGR 50

RESULT 7
US-08-314-309A-19
; Sequence 19, Application US/08314309A
; Patent No. 5677141
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: FUKAGAWA, MASAO
; APPLICANT: IWAMI, MORITA
; APPLICANT: ARAMORI, ICHIRO
; APPLICANT: KOJO, HITOSHI
; TITLE OF INVENTION: PROCESS FOR PRODUCING 7-AMINOCEPHEM
; TITLE OF INVENTION: COMPOUND OR SALTS THEREOF
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,309A
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; FILING DATE: 30-SEP-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/631,906
 ; FILING DATE: 21-DEC-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Oblon, NO. 5677141man F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 18-863-0 CONT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 413-3000
 ; TELEFAX: (703) 413-2220
 ; TELEX: 248855 OPAT UR
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 341 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-314-309A-19

Query Match 90.0% Score 27; DB 1; Length 341;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6
 Db 301 AGTVGR 306

RESULT 8
 US-09-134-001C-2895
 ; Sequence 2895, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GPC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 2895
 ; LENGTH: 425
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 ; US-09-134-001C-2895

Query Match 90.0% Score 27; DB 4; Length 425;
 Best Local Similarity 83.3%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6
 Db 73 TGTVGR 78

RESULT 9
 US-08-557-210A-3
 ; Sequence 3, Application US/08557210A
 ; Patent No. 6114146
 ; GENERAL INFORMATION:
 ; APPLICANT: Herlitschka, Sabine
 ; APPLICANT: Schlokot, Uwe
 ; APPLICANT: Falkner, Falko Guenther
 ; APPLICANT: Dörner, Friedrich
 ; TITLE OF INVENTION: An expression plasmid, a fusion protein, a method of producing foreign
 ; TITLE OF INVENTION: transfected eukaryotic cell line, a method of producing foreign
 ; TITLE OF INVENTION: proteins, a foreign protein preparation as well as a pharmaceu

; TITLE OF INVENTION: composition
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/557,210A
 ; FILING DATE: 14-NOV-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: A 2099/94
 ; FILING DATE: 14-NOV-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ISACSON, John P.
 ; REGISTRATION NUMBER: 33,715
 ; REFERENCE/DOCKET NUMBER: 040433/0142/SOPA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 524 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-557-210A-3

Query Match 90.0% Score 27; DB 3; Length 524;
 Best Local Similarity 83.3%; Pred. No. 3.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6
 Db 484 AGTVGR 489

RESULT 10
 US-08-557-210A-4
 ; Sequence 4, Application US/08557210A
 ; Patent No. 6114146
 ; GENERAL INFORMATION:
 ; APPLICANT: Herlitschka, Sabine
 ; APPLICANT: Schlokot, Uwe
 ; APPLICANT: Falkner, Falko Guenther
 ; APPLICANT: Dörner, Friedrich
 ; TITLE OF INVENTION: An expression plasmid, a fusion protein, a method of producing for
 ; TITLE OF INVENTION: transfected eukaryotic cell line, a method of producing for
 ; TITLE OF INVENTION: proteins, a foreign protein preparation as well as a pharma
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/557,210A
;; FILING DATE: 14-NOV-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: A 2099/94
;; FILING DATE: 14-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ISACSON, John P.
;; REGISTRATION NUMBER: 33,715
;; REFERENCE/DOCKET NUMBER: 040433/0142/SOPA
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 539 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 192..196
;; OTHER INFORMATION: /note= "Glycin Spacer"
US-08-557-210A-4

Query Match 90.0%; Score 27; DB 3; Length 539;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
Db 499 AGTVGR 504

RESULT 11
US-08-557-210A-5
;; Sequence 5, Application US/08557210A
;; Patent No. 6114146
;; GENERAL INFORMATION:
;; APPLICANT: Herlitschka, Sabine
;; APPLICANT: Schlokot, Uwe
;; APPLICANT: Falkner, Falko Guenther
;; APPLICANT: Dörner, Friedrich
;; TITLE OF INVENTION: An expression plasmid, a fusion protein, a
;; TITLE OF INVENTION: transfectant eukaryotic cell line, a method of producing foreign
;; TITLE OF INVENTION: proteins, a foreign protein preparation as well as a pharmaceu
;; TITLE OF INVENTION: composition
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/557,210A
;; FILING DATE: 14-NOV-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: A 2099/94
;; FILING DATE: 14-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ISACSON, John P.
;; REGISTRATION NUMBER: 33,715

;; REFERENCE/DOCKET NUMBER: 040433/0142/SOPA
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 539 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 190..194
;; OTHER INFORMATION: /note= "Prolin Spacer"
US-08-557-210A-5

Query Match 90.0%; Score 27; DB 3; Length 539;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
Db 499 AGTVGR 504

RESULT 12
US-08-474-169-8
;; Sequence 8, Application US/08474169
;; Patent No. 5851796
;; GENERAL INFORMATION:
;; APPLICANT: Schatz, David G.
;; TITLE OF INVENTION: An Autoregulatory Tetracycline-Regulated
;; TITLE OF INVENTION: System for Inducible Gene Expression in Eucaryotes
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;; STREET: 1100 New York Ave. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/474,169
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 561 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-474-169-8

Query Match 90.0%; Score 27; DB 2; Length 561;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
Db 6 SGTVGR 11

RESULT 13

PCT-US91-08442-2
; Sequence 2, Application PC/TUS9108442
; GENERAL INFORMATION:
; APPLICANT: Lupion, Stephen D.
; TITLE OF INVENTION: Bifunctional Selectable Fusion Genes
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08442
; FILING DATE: 19911112
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2702-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)587-0606
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 691 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-08442-2

Query Match 90.0%; Score 27; DB 5; Length 691;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6
Db 301 AGTVGR 306

RESULT 14
US-08-434-730-16
; Sequence 16, Application US/08434730
; Patent No. 5637463
; GENERAL INFORMATION:
; APPLICANT: Dalton, Stephen
; APPLICANT: Kochan, Jarema P
; APPLICANT: Osborne, Mark A
; TITLE OF INVENTION: METHOD TO DETECT PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,730
; FILING DATE: 04-MAY-1995

CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Semionow, Raina
; REGISTRATION NUMBER: 39022
; REFERENCE/DOCKET NUMBER: 9069
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)235-4391
; TELEFAX: (201)235-2363
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-434-730-16

Query Match 90.0%; Score 27; DB 1; Length 756;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6
Db 206 AGTVGR 211

RESULT 15
US-08-602-999A-190
; Sequence 190, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-190

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:30:59 ; Search time 13.5385 Seconds
(without alignments)
59.054 Million cell updates/sec

Title: US-09-673-490B-1
Perfect score: 30
Sequence: 1 SGTGR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	21 AAY43707	Sequence of the fo
2	30	100.0	27	21 AAY43711	Amino acid sequenc
3	30	100.0	27	21 AAY43712	Amino acid sequenc
4	30	100.0	27	21 AAY43713	Amino acid sequenc
5	30	100.0	27	21 AAY43718	Amino acid sequenc
6	30	100.0	27	21 AAY43719	Amino acid sequenc
7	30	100.0	27	21 AAY43720	Amino acid sequenc
8	30	100.0	27	21 AAY43722	Amino acid sequenc
9	30	100.0	27	21 AAY43723	Amino acid sequenc
10	30	100.0	27	21 AAY43724	Amino acid sequenc

11	30	100.0	27	21 AAY43725	Amino acid sequenc
12	30	100.0	27	21 AAY43726	Amino acid sequenc
13	30	100.0	27	21 AAY43728	Amino acid sequenc
14	30	100.0	27	21 AAY43731	Amino acid sequenc
15	30	100.0	27	21 AAY43732	Amino acid sequenc
16	30	100.0	27	21 AAY43733	Amino acid sequenc
17	30	100.0	27	21 AAY43734	Amino acid sequenc
18	30	100.0	27	21 AAY43735	Amino acid sequenc
19	30	100.0	27	21 AAY43736	Amino acid sequenc
20	30	100.0	27	21 AAY43727	Amino acid sequenc
21	30	100.0	28	21 AAY43729	Amino acid sequenc
22	30	100.0	28	21 AAY43730	Amino acid sequenc
23	30	100.0	73	21 AAY43717	Amino acid sequenc
24	30	100.0	945	22 AAM51653	Arabidopsis thalia
25	30	100.0	1249	22 ABB71313	Drosophila melanog
26	30	100.0	1402	19 AAW64150	Lettuce resistance
27	30	100.0	1402	23 AAB95463	Lettuce pest resis
28	29	96.7	119	22 ABB71029	Drosophila melanog
29	29	96.7	234	23 ABP40101	Staphylococcus epi
30	29	96.7	385	22 AAB88544	Haemophilus influe
31	29	96.7	385	23 AAU91475	Haemophilus influe
32	29	96.7	745	16 AAR76110	Human ALD. Homo s
33	29	96.7	745	17 AAW03560	Human adrenoleucod
34	27	90.0	50	22 AAU67194	Propionibacterium
35	27	90.0	52	22 AAU55365	Propionibacterium
36	27	90.0	71	22 AAU52548	Propionibacterium
37	27	90.0	80	22 AAU57304	Propionibacterium
38	27	90.0	95	22 AAG77810	Human HDPAO68 seri
39	27	90.0	123	22 AAU63711	Propionibacterium
40	27	90.0	150	20 AAY28560	Partial Wnt-10a po
41	27	90.0	252	18 AAW28247	Amino acid sequenc
42	27	90.0	260	23 ABB76427	Human Ras protein
43	27	90.0	296	22 ABB69021	Drosophila melanog
44	27	90.0	309	22 AAB93912	Human protein sequ
45	27	90.0	339	6 AAP50324	Sequence of the 1a

ALIGNMENTS

RESULT 1
AAY43707
ID AAY43707 standard; peptide; 6 AA.
AC AAY43707;
XX
XX
XX
DT 11-FEB-2000 (first entry)

Sequence of the fourth loop of an omega conotoxin.

Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
neuronal damage reduction; ischemia; analgesia; opiate analgesia;
schizophrenia; stimulant induced psychosis; hypertension; inflammation;
bronchotension; neuropathic pain; voltage sensitive calcium channel.

Conus catus.

WO9954350-A1.

28-OCT-1999.

16-APR-1999; 99WO-AU00288.

16-APR-1998; 98AU-0002989.

01-FEB-1999; 99AU-0008419.

(UYQU) UNIV QUEENSLAND.

Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

WPI; 2000-013226/01.

Novel peptides used for the treatment of disorders and diseases where

PT blockage of the N-type calcium channels is required -
 PS Claim 1; Page 44; 81pp; English.
 CC The present sequence represents the fourth loop of an isolated,
 CC synthetic, or recombinant omega-conotoxin. Omega-conotoxins are
 CC isolated from venoms of predatory marine snails, and have a
 CC selectivity for N-type calcium channels over P/Q type channels, and so
 CC block N-type calcium channels. The omega-conotoxins of the invention
 CC can be used in any disease or disorder where blockage of N-type calcium
 CC channels is required, e.g. in the reduction of neuronal damage following
 CC ischemia, production of analgesia, or enhancement of opiate analgesia,
 CC in the treatment of schizophrenia, stimulant induced psychoses,
 CC hypertension, inflammation, and diseases which cause bronchotension,
 CC and also in the inhibition of progression of neuropathic pain. They can
 CC also be used in a screen to identify compounds with activity at N-type
 CC voltage sensitive calcium channels.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 30; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SGTGVR 6
 Db 1 SGTGVR 6
 RESULT 2
 AAY43711
 ID AAY43711 standard; peptide: 27 AA.
 AC AAY43711;
 XX
 DT 11-FEB-2000 (first entry)
 DE
 DE Amino acid sequence of an omega-conotoxin CVID.
 XX
 KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX
 OS Conus catus.
 XX
 PN WO9954350-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 16-APR-1999; 99WO-AU00288.
 XX
 PR 16-APR-1998; 98AU-0002989.
 XX
 PR 01-FEB-1999; 99AU-0008419.
 XX
 PA (UYQU) UNIV QUEENSLAND.
 XX
 PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX
 DR WPI; 2000-013226/01.
 XX
 PT Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -
 XX
 PS Claim 6; Page 45; 81pp; English.
 CC The present sequence represents an omega-conotoxin. Omega-conotoxins
 CC are isolated from venoms of predatory marine snails, and have a
 CC selectivity for N-type calcium channels over P/Q type channels, and so
 CC block N-type calcium channels. The omega-conotoxins of the invention
 CC can be used in any disease or disorder where blockage of N-type calcium
 CC channels is required, e.g. in the reduction of neuronal damage following
 CC ischemia, production of analgesia, or enhancement of opiate analgesia,

CC in the treatment of schizophrenia, stimulant induced psychoses,
 CC hypertension, inflammation, and diseases which cause bronchotension,
 CC and also in the inhibition of progression of neuropathic pain. They can
 CC also be used in a screen to identify compounds with activity at N-type
 CC voltage sensitive calcium channels.
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 30; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SGTGVR 6
 Db 21 SGTGVR 26
 RESULT 3
 AAY43712
 ID AAY43712 standard; peptide: 27 AA.
 AC AAY43712;
 XX
 DT 11-FEB-2000 (first entry)
 DE
 DE Amino acid sequence of an omega-conotoxin R10-CVID.
 XX
 KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
 XX
 OS Synthetic.
 OS Conus catus.
 XX
 PN WO9954350-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 16-APR-1999; 99WO-AU00288.
 XX
 PR 16-APR-1998; 98AU-0002989.
 XX
 PR 01-FEB-1999; 99AU-0008419.
 XX
 PA (UYQU) UNIV QUEENSLAND.
 XX
 PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 XX
 DR WPI; 2000-013226/01.
 XX
 PT Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -
 XX
 PS Claim 6; Page 45; 81pp; English.
 CC The present sequence represents a modified version of omega-conotoxin
 CC CVID (see AAY43712). Omega-conotoxins are isolated from venoms of
 CC predatory marine snails, and have a selectivity for N-type calcium
 CC channels over P/Q type channels, and so block N-type calcium channels.
 CC The omega-conotoxins of the invention can be used in any disease or
 CC disorder where blockage of N-type calcium channels is required, e.g. in
 CC the reduction of neuronal damage following ischemia, production of
 CC analgesia, or enhancement of opiate analgesia, in the treatment of
 CC schizophrenia, stimulant induced psychoses, hypertension, inflammation,
 CC and diseases which cause bronchotension, and also in the inhibition of
 CC progression of neuropathic pain. They can also be used in a screen to
 CC identify compounds with activity at N-type voltage sensitive calcium
 CC channels.
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 30; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 15;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
 DB 21 SGTVGR 26

RESULT 4

AA43713
 ID AAY43713 standard; peptide; 27 AA.

AC AAY43713;

DT 11-FEB-2000 (first entry)

DE Amino acid sequence of omega-conotoxin D9R10-CVID.

KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

OS Synthetic.

OS Conus catus.

PN WO9954350-A1.

XX 28-OCT-1999.

PF 16-APR-1999; 99WO-AU00288.

XX 16-APR-1999; 98AU-0002989.

PR 01-FEB-1999; 99AU-0008419.

XX (UYQU) UNIV QUEENSLAND.

PA Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

PI WPI; 2000-013226/01.

XX Novel peptides used for the treatment of disorders and diseases where

PT blockage of the N-type calcium channels is required -

PS Claim 6; Page 45; 81pp; English.

XX The present sequence represents a modified version of omega-conotoxin
 CC CVID (see AAY43712). Omega-conotoxins are isolated from venoms of
 CC predatory marine snails, and have a selectivity for N-type calcium
 CC channels over P/Q type channels, and so block N-type calcium channels.
 CC The omega-conotoxins of the invention can be used in any disease or
 CC disorder where blockage of N-type calcium channels is required, e.g. in
 CC the reduction of neuronal damage following ischemia, production of
 CC analgesia, or enhancement of opiate analgesia, in the treatment of
 CC schizophrenia, stimulant induced psychoses, hypertension, inflammation,
 CC and diseases which cause bronchotension, and also in the inhibition of
 CC progression of neuropathic pain. They can also be used in a screen to
 CC identify compounds with activity at N-type voltage sensitive calcium
 CC channels.

XX Sequence 27 AA;

QY Query Match 100.0%; Score 30; DB 21; Length 27;

DB Best Local Similarity 100.0%; Pred. No. 15;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6

DB 21 SGTVGR 26

RESULT 5

AA43718
 ID AAY43718 standard; peptide; 27 AA.

XX AAY43718;

DT 11-FEB-2000 (first entry)

DE Amino acid sequence of an omega-conotoxin derivative of CVID.

KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

OS Synthetic.

OS Conus catus.

PN WO9954350-A1.

XX 28-OCT-1999.

PF 16-APR-1999; 99WO-AU00288.

XX 16-APR-1999; 98AU-0002989.

PR 01-FEB-1999; 99AU-0008419.

XX (UYQU) UNIV QUEENSLAND.

PA Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

PI WPI; 2000-013226/01.

XX Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -

PS Claim 6; Page 45; 81pp; English.

XX AAY43718-36 represent derivatives of omega-conotoxin CVID.

CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.

XX Sequence 27 AA;

QY Query Match 100.0%; Score 30; DB 21; Length 27;

DB Best Local Similarity 100.0%; Pred. No. 15;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6

DB 21 SGTVGR 26

RESULT 6

AA43719
 ID AAY43719 standard; peptide; 27 AA.

AC AAY43719;

DT 11-FEB-2000 (first entry)

DE Amino acid sequence of an omega-conotoxin derivative of CVID.

KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

PS Claim 6; Page 45; 8lpp; English.

XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.

XX SQ Sequence 27 AA;

Query Match 100.0%; Score 30; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
 DB 21 SGTVGR 26
 |||||

RESULT 9

AAY43723

ID AAY43723 standard; peptide; 27 AA.

XX AC AAY43723;

XX DT 11-FEB-2000 (first entry)

XX DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;

KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

OS Synthetic.

OS Conus catus.

PN WO9954350-A1.

XX PD 28-OCT-1999.

XX PF 16-APR-1999; 99WO-AU00288.

XX PR 16-APR-1998; 98AU-0002989.

XX PR 01-FEB-1999; 99AU-0008419.

PA (UYOU) UNIV QUEENSLAND.

XX PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX WPI: 2000-013226/01.

XX PT Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -

XX PS Claim 6; Page 45; 8lpp; English.

XX CC AAY43718-36 represent derivatives of omega-conotoxin CVID.

CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause

CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.

XX SQ Sequence 27 AA;

Query Match 100.0%; Score 30; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6

DB 21 SGTVGR 26

|||||

RESULT 10

AAY43724

ID AAY43724 standard; peptide; 27 AA.

XX AC AAY43724;

XX DT 11-FEB-2000 (first entry)

XX DE Amino acid sequence of an omega-conotoxin derivative of CVID.

XX KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

OS Synthetic.

OS Conus catus.

PN WO9954350-A1.

XX PD 28-OCT-1999.

XX PF 16-APR-1999; 99WO-AU00288.

XX PR 16-APR-1998; 98AU-0002989.

XX PR 01-FEB-1999; 99AU-0008419.

PA (UYOU) UNIV QUEENSLAND.

XX PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX WPI: 2000-013226/01.

XX PT Novel peptides used for the treatment of disorders and diseases where
 PT blockage of the N-type calcium channels is required -

XX PS Claim 6; Page 45; 8lpp; English.

XX CC AAY43718-36 represent derivatives of omega-conotoxin CVID.

CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.

XX SQ Sequence 27 AA;

Query Match 100.0%; Score 30; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6

```

Db      21 SGTVGR 26
|||||
RESULT 11
AAV43725
ID      AAV43725 standard; peptide: 27 AA.
XX
AC      AAV43725;
XX
DT      11-FEB-2000 (first entry)
XX
DE      Amino acid sequence of an omega-conotoxin derivative of CVID.
XX
KW      Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW      neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
KW      schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW      bronchotension; neuropathic pain; voltage sensitive calcium channel.
XX
OS      Synthetic.
OS      Conus catus.
XX
PN      WO9954350-A1.
XX
PD      28-OCT-1999.
XX
PF      16-APR-1999; 99WO-AU00288.
XX
PR      16-APR-1998; 98AU-0002989.
PR      01-FEB-1999; 99AU-0008419.
XX
PA      (UYQU ) UNIV QUEENSLAND.
XX
PI      Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX
WPI: 2000-013226/01.
XX
Novel peptides used for the treatment of disorders and diseases where
blockage of the N-type calcium channels is required
XX
Claim 6; Page 45; 81pp; English.
XX
AAV43718-36 represent derivatives of omega-conotoxin CVID.
CC
Omega-conotoxins are isolated from venoms of predatory marine snails, and
CC
have a selectivity for N-type calcium channels over P/Q type channels,
CC
and so block N-type calcium channels. The omega-conotoxins of the
CC
invention can be used in any disease or disorder where blockage of N-type
CC
calcium channels is required, e.g. in the reduction of neuronal damage
CC
following ischemia, production of analgesia, or enhancement of opiate
CC
analgesia, in the treatment of schizophrenia, stimulant induced
CC
psychoses, hypertension, inflammation, and diseases which cause
CC
bronchotension, and also in the inhibition of progression of neuropathic
CC
pain. They can also be used in a screen to identify compounds with
CC
activity at N-type voltage sensitive calcium channels.
XX
SQ      Sequence 27 AA;
Query Match 100.0%; Score 30; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 SGTVGR 6
Db      21 SGTVGR 26
|||||
RESULT 12
AAV43726
ID      AAV43726 standard; peptide: 27 AA.
XX
AC      AAV43726;
XX
DT      11-FEB-2000 (first entry)

```

```

XX      Amino acid sequence of an omega-conotoxin derivative of CVID.
DE
XX
KW      Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW      neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
KW      schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW      bronchotension; neuropathic pain; voltage sensitive calcium channel.
XX
OS      Synthetic.
OS      Conus catus.
XX
FH      Key Location/Qualifiers
FT      Misc-difference 5 /note= "D-form residue"
FT
XX
PN      WO9954350-A1.
XX
PD      28-OCT-1999.
XX
PF      16-APR-1999; 99WO-AU00288.
XX
PR      16-APR-1998; 98AU-0002989.
PR      01-FEB-1999; 99AU-0008419.
XX
PA      (UYQU ) UNIV QUEENSLAND.
XX
PI      Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX
WPI: 2000-013226/01.
XX
Novel peptides used for the treatment of disorders and diseases where
blockage of the N-type calcium channels is required
XX
Claim 6; Page 45; 81pp; English.
XX
AAV43718-36 represent derivatives of omega-conotoxin CVID.
CC
Omega-conotoxins are isolated from venoms of predatory marine snails, and
CC
have a selectivity for N-type calcium channels over P/Q type channels,
CC
and so block N-type calcium channels. The omega-conotoxins of the
CC
invention can be used in any disease or disorder where blockage of N-type
CC
calcium channels is required, e.g. in the reduction of neuronal damage
CC
following ischemia, production of analgesia, or enhancement of opiate
CC
analgesia, in the treatment of schizophrenia, stimulant induced
CC
psychoses, hypertension, inflammation, and diseases which cause
CC
bronchotension, and also in the inhibition of progression of neuropathic
CC
pain. They can also be used in a screen to identify compounds with
CC
activity at N-type voltage sensitive calcium channels.
XX
SQ      Sequence 27 AA;
Query Match 100.0%; Score 30; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 SGTVGR 6
Db      21 SGTVGR 26
|||||
RESULT 13
AAV43728
ID      AAV43728 standard; peptide: 27 AA.
XX
AC      AAV43728;
XX
DT      11-FEB-2000 (first entry)
XX
DE      Amino acid sequence of an omega-conotoxin derivative of CVID.
XX
KW      Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW      neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
KW      schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW      bronchotension; neuropathic pain; voltage sensitive calcium channel.

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XX OS Synthetic.
XX OS Conus catus.
XX
XX Key Location/Qualifiers
XX Misc-difference 27
XX FT /note= "free carboxyl at the C-terminal"
XX
XX W09954350-A1.
XX PN
XX PD 28-OCT-1999.
XX PF 16-APR-1999; 99WO-AU00288.
XX PR 16-APR-1998; 98AU-0002989.
XX PR 01-FEB-1999; 99AU-0008419.
XX PA (UYOU ) UNIV QUEENSLAND.
XX PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX WPI; 2000-013226/01.
XX
XX Novel peptides used for the treatment of disorders and diseases where
XX blockage of the N-type calcium channels is required -
XX
XX Claim 6; Page 45; 81pp; English.
XX
XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
XX Omega-conotoxins are isolated from venoms of predatory marine snails, and
XX have a selectivity for N-type calcium channels over P/Q type channels,
XX and so block N-type calcium channels. The omega-conotoxins of the
XX invention can be used in any disease or disorder where blockage of N-type
XX calcium channels is required, e.g. in the reduction of neuronal damage
XX following ischemia, production of analgesia, or enhancement of opiate
XX analgesia, in the treatment of schizophrenia, stimulant induced
XX psychoses, hypertension, inflammation, and diseases which cause
XX bronchotension, and also in the inhibition of progression of neuropathic
XX pain. They can also be used in a screen to identify compounds with
XX activity at N-type voltage sensitive calcium channels.
XX
XX Query Match 100.0%; Score 30; DB 21; Length 27;
XX Best Local Similarity 100.0%; Pred. No. 15;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SGTVGR 6
XX DB 21 SGTVGR 26
XX
XX RESULT 14
XX AAY43731
XX ID AAY43731 standard; peptide; 27 AA.
XX
XX AC AAY43731;
XX
XX DT 11-FEB-2000 (first entry)
XX
XX DE Amino acid sequence of an omega-conotoxin derivative of CVID.
XX
XX KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
XX neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
XX KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
XX KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
XX
XX OS Synthetic.
XX OS Conus catus.
XX
XX Key Location/Qualifiers
XX Modified-site 12
XX FT /label= Nle
XX

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FT /note= "norleucine"
XX
XX W09954350-A1.
XX PN
XX PD 28-OCT-1999.
XX PF 16-APR-1999; 99WO-AU00288.
XX PR 16-APR-1998; 98AU-0002989.
XX PR 01-FEB-1999; 99AU-0008419.
XX PA (UYOU ) UNIV QUEENSLAND.
XX PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX WPI; 2000-013226/01.
XX
XX Novel peptides used for the treatment of disorders and diseases where
XX blockage of the N-type calcium channels is required -
XX
XX Claim 6; Page 46; 81pp; English.
XX
XX AAY43718-36 represent derivatives of omega-conotoxin CVID.
XX Omega-conotoxins are isolated from venoms of predatory marine snails, and
XX have a selectivity for N-type calcium channels over P/Q type channels,
XX and so block N-type calcium channels. The omega-conotoxins of the
XX invention can be used in any disease or disorder where blockage of N-type
XX calcium channels is required, e.g. in the reduction of neuronal damage
XX following ischemia, production of analgesia, or enhancement of opiate
XX analgesia, in the treatment of schizophrenia, stimulant induced
XX psychoses, hypertension, inflammation, and diseases which cause
XX bronchotension, and also in the inhibition of progression of neuropathic
XX pain. They can also be used in a screen to identify compounds with
XX activity at N-type voltage sensitive calcium channels.
XX
XX Query Match 100.0%; Score 30; DB 21; Length 27;
XX Best Local Similarity 100.0%; Pred. No. 15;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SGTVGR 6
XX DB 21 SGTVGR 26
XX
XX RESULT 15
XX AAY43732
XX ID AAY43732 standard; peptide; 27 AA.
XX
XX AC AAY43732;
XX
XX DT 11-FEB-2000 (first entry)
XX
XX DE Amino acid sequence of an omega-conotoxin derivative of CVID.
XX
XX KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
XX neuronal damage reduction; ischemia; analgesia; opiate analgesia; CVID;
XX KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
XX KW bronchotension; neuropathic pain; voltage sensitive calcium channel.
XX
XX OS Synthetic.
XX OS Conus catus.
XX
XX Key Location/Qualifiers
XX Modified-site 12
XX FT /label= Nle
XX FT /note= "norleucine"
XX
XX W09954350-A1.
XX PN
XX PD 28-OCT-1999.
XX

```

PF 16-APR-1999; 99WO-AU00288.
 XX
 PR 16-APR-1998; 98AU-0002989.
 PR 01-FEB-1999; 99AU-0008419.
 XX
 XX (UYOU) UNIV QUEENSLAND.
 PA
 XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
 PI WPI; 2000-013226/01.
 XX
 DR Novel peptides used for the treatment of disorders and diseases where
 XX blockage of the N-type calcium channels is required -
 PT
 PS Claim 6; Page 46; 81pp; English.
 XX
 CC AAY43718-36 represent derivatives of omega-conotoxin CVID.
 CC Omega-conotoxins are isolated from venoms of predatory marine snails, and
 CC have a selectivity for N-type calcium channels over P/Q type channels,
 CC and so block N-type calcium channels. The omega-conotoxins of the
 CC invention can be used in any disease or disorder where blockage of N-type
 CC calcium channels is required, e.g. in the reduction of neuronal damage
 CC following ischemia, production of analgesia, or enhancement of opiate
 CC analgesia, in the treatment of schizophrenia, stimulant induced
 CC psychoses, hypertension, inflammation, and diseases which cause
 CC bronchotension, and also in the inhibition of progression of neuropathic
 CC pain. They can also be used in a screen to identify compounds with
 CC activity at N-type voltage sensitive calcium channels.
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 30; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. NO. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGTVGR 6
 Db 21 SGTVGR 26
 Search completed: February 26, 2003, 08:36:50
 Job time : 15.5385 secs

Query Match 86.7%; Score 26; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTVGR 6
Db 2 GTVGR 6

Search completed: February 26, 2003, 08:41:03
Job time : 5.23077 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:32:19 ; Search time 20.9231 Seconds
(without alignments)
59.087 Million cell updates/sec

Title: US-09-673-490B-2
Perfect score: 31
Sequence: 1. SKLMYD 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	93.5	267	12 O8QTF9	O8qtf9 white spot
2	29	93.5	507	12 O8QY8	O8qy8 white spot
3	29	93.5	998	12 O9JLJ5	O9jlj5 spodoptera
4	29	93.5	1022	12 O9IBF6	O9ibf6 spodoptera
5	29	93.5	1535	12 O9ILK0	O9ilk0 white spot
6	28	90.3	146	16 O8RAL2	O8ral2 thermoanaer
7	28	90.3	722	5 O15983	O15983 halocynthia
8	28	90.3	927	16 O9KPC0	O9kpc0 vibrio chol
9	27	87.1	108	12 O84641	O84641 paramecium
10	27	87.1	154	12 O9YMU9	O9ymu9 lymantria d
11	27	87.1	196	9 O8SBT6	O8sbt6 cyanophage
12	27	87.1	240	10 O9FPE3	O9fpe3 arbidopsis
13	27	87.1	249	10 O94FX0	O94fx0 glycine max
14	27	87.1	250	10 O94FX1	O94fx1 glycine max
15	27	87.1	250	16 O99W24	O99w24 staphylococ
16	27	87.1	259	5 O8SUG2	O8sug2 encephalito

17	27	87.1	278	10	O94FW7	O94fw7 lycopersico
18	27	87.1	282	10	O48782	O48782 arbidopsis
19	27	87.1	285	10	O9C9L4	O9c9l4 arbidopsis
20	27	87.1	318	16	O8XJ39	O8xj39 escherichia
21	27	87.1	322	16	O8Z0A8	O8z0a8 anabaena sp
22	27	87.1	337	16	O8XP45	O8xp45 clostridium
23	27	87.1	384	16	O9CIS4	O9cis4 lactococcus
24	27	87.1	402	16	O97HX4	O97hx4 clostridium
25	27	87.1	424	5	O9V9V0	O9v9v0 drosophila
26	27	87.1	432	10	O9SBK5	O9sbk5 triticum ae
27	27	87.1	459	13	O57578	O57578 xenopus lae
28	27	87.1	460	5	O9VV72	O9vv72 drosophila
29	27	87.1	467	5	O96421	O96421 drosophila
30	27	87.1	467	5	O8SYN4	O8syn4 drosophila
31	27	87.1	479	10	O9M8R8	O9m8r8 arbidopsis
32	27	87.1	479	10	O9ZTW6	O9ztw6 triticum ae
33	27	87.1	509	11	O9D094	O9d094 mus musculu
34	27	87.1	509	11	O8VDX8	O8vdx8 mus musculu
35	27	87.1	520	11	O61078	O61078 mus musculu
36	27	87.1	522	5	O9VWT1	O9vwt1 drosophila
37	27	87.1	538	3	O43011	O43011 schizosacch
38	27	87.1	540	5	O17826	O17826 caenorhabdi
39	27	87.1	562	16	P74611	P74611 synechocyst
40	27	87.1	696	5	O17479	O17479 hyalophora
41	27	87.1	723	5	O97353	O97353 toxoplasma
42	27	87.1	815	5	O61517	O61517 drosophila
43	27	87.1	854	5	O960G8	O960g8 drosophila
44	27	87.1	854	5	O9VPW1	O9vpw1 drosophila
45	27	87.1	859	16	O9JYQ8	O9jyq8 neisseria m

ALIGNMENTS

RESULT 1

O8QTF9	PRELIMINARY;	PRT;	267 AA.
ID	O8QTF9		
AC	O8QTF9;		
DT	01-JUN-2002 (TrEMBLrel. 21, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	WSSV082.		
OS	White spot syndrome virus (WSSV).		
OC	Viruses; unclassified viruses.		
OX	NCBI_TaxID=92652;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=TAIWAN;		
RX	MEDLINE=20517548; PubMed=11062040;		
RA	Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,		
RA	Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;		
RT	"Identification and characterization of a shrimp white spot syndrome virus (WSSV) gene that encodes a novel chimeric polypeptide of cellular-type thymidine kinase and thymidylate kinase."		
RT	Virolgy 277:100-110(2000).		
RL			

Query Match 93.5%; Score 29; DB 12; Length 267;
 Best Local Similarity 83.3%; Pred. No. 53;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMDYD 6
 ||:||||
 Db 74 SKIMYD 79

RESULT 2

Q80QY8 PRELIMINARY; PRT; 507 AA.
 AC Q80QY8;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE VP507 (Fragment).
 OS White spot syndrome virus (WSSV).
 OC Viruses; unclassified viruses.
 OX NCBI_TaxID=92652;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Huang C., Hew C.L.;
 RT "The VP507 gene from shrimp white spot syndrome virus.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 FR EMBL; AF493146; ANM12817.1; -;
 DT NON_TER 507
 FT SEQUENCE 507 AA; 57032 MW; 8A2C19698354A606 CRC64;

Query Match 93.5%; Score 29; DB 12; Length 507;
 Best Local Similarity 83.3%; Pred. No. 99;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMDYD 6
 ||:||||
 Db 314 SKIMYD 319

RESULT 3

Q9J1J5 PRELIMINARY; PRT; 998 AA.
 AC Q9J1J5;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE DNA polymerase.
 GN POL.
 OS Spodoptera littoralis nuclear polyhedrosis virus (SLNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=10456;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang J., Levin D.B.;
 RT "Identification, Transcription, Sequence, and Phylogenetic Analysis of the Type B Nucleopolyhedrovirus of Spodoptera littoralis (SLNPV) DNA polymerase Gene.";
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RL CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N DIPHOSPHATE + [DNA](N).
 CC -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
 DR EMBL; AF215639; AAF61904.1; -;
 DR InterPro; IPR002064; DNA_pol_B.
 DR Pfam; PF00136; DNA_pol_B; 1.
 DR Pfam; PF03104; DNA_pol_B_exo; 1.
 DR PRINTS; PR00106; DNAPOLB.
 DR SMART; SM00486; POLBc; 1.
 DR DNA replication; DNA-binding; DNA-directed DNA polymerase.
 SK SEQUENCE 998 AA; 114935 MW; B168E28520B1373F CRC64;

Query Match 93.5%; Score 29; DB 12; Length 998;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMDYD 6
 ||:||||
 Db 929 SKMMYD 934

RESULT 4

Q91BF6 PRELIMINARY; PRT; 1022 AA.
 AC Q91BF6;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE DNA polymerase.
 OS Spodoptera litura nucleopolyhedrovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=46242;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G2;
 RX MEDLINE=21425398; PubMed=11531416;
 RA Pang Y., Yu J., Wang L., Hu X., Bao W., Li G., Chen C., Han H., Hu S.,
 RA Yang H.;
 RT "Sequence Analysis of the Spodoptera litura Multicapsid Nucleopolyhedrovirus Genome.";
 RL Virology 287:391-404(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G2;
 RA Yu J., Wang L., Hu X., Pang Y.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N DIPHOSPHATE + [DNA](N).
 CC -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
 DR EMBL; AF25155; AAL01751.1; -;
 DR InterPro; IPR002064; DNA_pol_B.
 DR Pfam; PF00136; DNA_pol_B; 1.
 DR Pfam; PF03104; DNA_pol_B_exo; 1.
 KW DNA replication; DNA-binding; DNA-directed DNA polymerase.
 SQ SEQUENCE 1022 AA; 118030 MW; 5F1FA9CED83168DD CRC64;

Query Match 93.5%; Score 29; DB 12; Length 1022;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMDYD 6
 ||:||||
 Db 929 SKMMYD 934

RESULT 5

Q91LK0 PRELIMINARY; PRT; 1535 AA.
 AC Q91LK0;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE ORF40 (Wsv026).
 OS White spot syndrome virus (WSSV).
 OC Viruses; unclassified viruses.
 OX NCBI_TaxID=92652;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21342572; PubMed=11448154;
 RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
 RA Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Viak J.M.;
 RL "The white spot syndrome virus DNA genome sequence.";
 RL Virology 286:7-22(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,


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RA Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vlak J.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21548311; PubMed=11689662;
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RT "Complete genome sequence of the shrimp white spot bacilliform
virus.";
RL J. Virol. 75:11811-11820(2001).
RN [4]
RP SEQUENCE FROM N.A.
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF369029; AAK77709.1; -.
DR EMBL; AF332093; AAL33030.1; -.
SQ SEQUENCE 1535 AA; 172098 MW; 9871D4C4FFB27F29 CRC64;

Query Match 93.5%; Score 29; DB 12; Length 1535;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
   ||:||||
Db 1342 SKLMYD 1347

RESULT 6
QBRAL2
ID QBRAL2 PRELIMINARY; PRT; 146 AA.
AC QBRAL2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Transcriptional regulator.
GN MARR OR Trel201.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WB47 / JCM11007;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Yang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013082; AAM24431.1; -.
KW Complete proteome.
SQ SEQUENCE 146 AA; 16793 MW; 9438E7C9AE88E224 CRC64;

Query Match 90.3%; Score 28; DB 16; Length 146;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
   ||:||||
Db 7 SKLLYD 12

RESULT 7
O15983
ID O15983 PRELIMINARY; PRT; 722 AA.
AC O15983;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE A74 protein.
GN A74.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
```

```
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RA Takahashi H., Ishikawa G., Ueki K., Azumi K., Yokosawa H.;
RT "Cloning and tyrosine-phosphorylation of a novel invertebrate
immunocyte protein containing immunoreceptor tyrosine-based activation
motifs.";
RL J. Biol. Chem. 0:0-0(1997).
DR EMBL; AB007512; BAA22658.1; -.
SQ SEQUENCE 722 AA; 78921 MW; E13186B23B6D4520 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 722;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
   ||||:||||
Db 420 SKLLYD 425

RESULT 8
O9KPC0
ID O9KPC0 PRELIMINARY; PRT; 927 AA.
AC O9KPC0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Sensor histidine kinase/response regulator.
GN VC2453.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Colwell R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae.";
RL Nature 406:477-483(2000).
CC -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
CC -!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
DR EMBL; AE004315; AAF95595.1; -.
DR HSSP; P02933; 1BXD.
DR TIGR; VC2453; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003660; HAMP.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR004359; HIS_KIN_sig.
DR InterPro; IPR002570; Hpt.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01627; Hpt; 1.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00512; signal; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HisKA; 1.
DR SMART; SM00073; HPT; 1.
DR SMART; SM00073; HPT; 1.
DR SMART; SM00448; REC; 1.
KW Kinase; Phosphorylation; Sensory transduction; Transferase;
KW Complete proteome.
```

SQ SEQUENCE 927 AA; 103569 MW; 520DC4F2F7CA27BA CRC64;
 Query Match 90.3%; Score 28; DB 16; Length 927;
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
 I:||||
 Db 194 SRLMYD 199

RESULT 9
 Q84641 PRELIMINARY; PRT; 108 AA.
 AC Q84641;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE A327R protein.
 GN A327R.
 OS Paramesitium bursaria chlorella virus.1 (PBCV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
 OX NCBI_TaxID=10506;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96187795; PubMed=8614977;
 RA Lu Z., Li Y., Que Q., Kutish G.F., Rock D.L., Van Etten J.L.;
 RA "Analysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map
 RT positions 88 to 182.";
 RL Virology 216:102-123(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20013326; PubMed=10544099;
 RA Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
 RA Liseac A.D., Nickerson K.W., Van Etten J.L.;
 RT "Chlorella virus PBCV-1 encodes a functional homosperridine
 RT synthase.";
 RL Virology 263:254-262(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20478054; PubMed=11021991;
 RA Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
 RT "Characterization of a beta-1,3-glucanase encoded by Chlorella virus
 RT PBCV-1.";
 RL Virology 276:27-36(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Graves M.V., Van Etten J.L.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Graves M.V., Van Etten J.L.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RA Gurnon J.R., Graves M.V., Van Etten J.L.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U42580; AAC96695.1; -;
 SQ SEQUENCE 108 AA; 13081 MW; D87DE6E3C933AB5 CRC64;

Query Match 87.1%; Score 27; DB 12; Length 108;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 83.3%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
 I:||||
 Db 52 SKFMVD 57

RESULT 10
 Q9YMU9 PRELIMINARY; PRT; 154 AA.
 AC Q9YMU9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE LdOrf-25 peptide.
 OS Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OX NCBI_TaxID=10449;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99124785; PubMed=9887315;
 RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
 RA Slavicek J.M., Rohrmann G.F.;
 RT "Sequence and analysis of the genome of a baculovirus pathogenic for
 RT Lymantria dispar.";
 RL Virology 253:17-34(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kuzio J.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF081810; AAC70210.1; -;
 SQ SEQUENCE 154 AA; 18391 MW; 78D66650CE27A9CA CRC64;

Query Match 87.1%; Score 27; DB 12; Length 154;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
 I:||||
 Db 114 SKLYVD 119

RESULT 11
 Q8SBT6 PRELIMINARY; PRT; 196 AA.
 AC Q8SBT6;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Capsid assembly protein (Fragment).
 GN G20.
 OS cyanophage clone SS4716.
 OC Viruses; environmental samples.
 OX NCBI_TaxID=156806;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhong Y., Chen F., Wilhelm S.W., Poorvin L., Hodson R.E.;
 RA "Phylogenetic Diversity of Marine Cyanophage Isolates and Natural
 RT Virus Communities as Revealed by Sequences of Viral Capsid Assembly
 RT Protein Gene g20.";
 RL Appl. Environ. Microbiol. 68:1576-1584(2002).
 DR EMBL; AY028050; AAK31747.1; -;
 FT NON_TER 1
 FT NON_TER 196
 SQ SEQUENCE 196 AA; 23057 MW; 93951F5354455249 CRC64;

Query Match 87.1%; Score 27; DB 9; Length 196;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SKLMD 6
DB 28 SKLVD 33

RESULT 12
Q9FPE3 ID Q9FPE3 PRELIMINARY; PRT; 240 AA.
AC Q9FPE3;
DT 01-MAR-2001 (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE Putative heme oxygenase 1 (HOL) protein (At2g26670/F18A8.4).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Sakano H., Liu S.X., Pham P.K., Yamada K., Banh J., Etgu P., Lee J.M.,
RA Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full Length cDNA of gene F18A8.4/At2g26670 (GI:4883666).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene F18A8.4/At2g26670 (GI:4883666).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Shinn P.,
RA Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327418; AAG42008.1; -
DR EMBL; AF361100; AAK27725.1; -
DR EMBL; AF375414; AAK52998.1; -
SQ SEQUENCE 240 AA; 27969 MW; 20E210ED591B8AEE CRC64;

Query Match 87.1%; Score 27; DB 10; Length 240;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMD 6
DB 81 SKLVD 86

RESULT 13
Q94FX0 ID Q94FX0 PRELIMINARY; PRT; 249 AA.
AC Q94FX0;
DT 01-DEC-2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DE Heme oxygenase 3 (Fragment).
OS Homo sapiens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Davis S.J., Bhoo S.H., Durski A.M., Walker J.M., Vierstra R.D.;
RT "The heme-oxygenase family required for phytochrome chromophore
biosynthesis is necessary for proper photomorphogenesis in higher
plants.";
RL Plant Physiol. 126:656-669(2001).
DR EMBL; AF320025; AAK63009.1; -
FT NON_TER 1
SQ SEQUENCE 249 AA; 28319 MW; 203BE0A22C455E22 CRC64;

Query Match 87.1%; Score 27; DB 10; Length 249;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMD 6
DB 90 SKLVD 95

RESULT 14
Q94FX1 ID Q94FX1 PRELIMINARY; PRT; 250 AA.
AC Q94FX1;
DT 01-DEC-2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Heme oxygenase 1 (Fragment).
OS Homo sapiens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Davis S.J., Bhoo S.H., Durski A.M., Walker J.M., Vierstra R.D.;
RT "The heme-oxygenase family required for phytochrome chromophore
biosynthesis is necessary for proper photomorphogenesis in higher
plants.";
RL Plant Physiol. 126:656-669(2001).
DR EMBL; AF320024; AAK63008.1; -
FT NON_TER 1
SQ SEQUENCE 250 AA; 28544 MW; E0241C35ED1F5F1F CRC64;

Query Match 87.1%; Score 27; DB 10; Length 250;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMD 6
DB 91 SKLVD 96

RESULT 15
Q99W24 ID Q99W24 PRELIMINARY; PRT; 250 AA.
AC Q99W24;
DT 01-JUN-2001 (TREMREL. 17, Created)
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
DT 01-MAR-2002 (TREMREL. 20, Last annotation update)
DE Hypothetical protein SAV0587.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
```

RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Oi Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003359; BAB56749.1;
 DR EMBL; AP003131; BAB41776.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 250 AA; 29390 MW; B991C3DB917531E0 CRC64;

Query Match 87.1%; Score 27; DB 16; Length 250;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 KIMYD 6
 |||||
 Db 167 KIMYD 171

Search completed: February 26, 2003, 08:39:44
 Job time : 23.9231 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:31:34 ; Search time 2.92308 seconds
(without alignments)
85.136 Million cell updates/sec

Title: US-09-673-490B-2

Perfect score: 31

Sequence: 1 SKLMYD 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	26	1 CXOC_CONCT	P58919 conus catus
2	31	100.0	73	1 CXOD_CONCT	P58920 conus catus
3	28	90.3	71	1 CXOA_CONMA	P05484 conus magus
4	28	90.3	113	1 YEG3_CAMJE	Q9pmj7 campylobact
5	28	90.3	389	1 SERC_SCHPO	Q10349 schizosacch
6	28	90.3	460	1 RAS7_YEAST	P25301 saccharomyc
7	28	90.3	974	1 SINA_YEAST	P32259 saccharomyc
8	27	87.1	173	1 YCF3_FORPU	P51258 porphyra pu
9	27	87.1	235	1 YJBM_ECOLI	P32694 escherichia
10	27	87.1	275	1 NRTB_SYNY3	P37451 synechocyst
11	27	87.1	360	1 VE2_HPV70	P50773 human papil
12	27	87.1	364	1 SERC_DROME	Q9van0 drosophila
13	27	87.1	494	1 SYH_ORYSA	P93422 oryza sativ
14	27	87.1	502	1 WASP_HUMAN	P42768 homo sapien
15	27	87.1	509	1 SYH_HUMAN	P12081 homo sapien
16	27	87.1	509	1 SYH_MOUSE	Q61035 mus musculu
17	27	87.1	519	1 SYH_FUGRU	P70076 fuigu rubrip
18	27	87.1	520	1 WASP_MOUSE	P70315 mus musculu
19	27	87.1	566	1 YJ19_SYNY3	P73121 synechocyst
20	27	87.1	773	1 GYRB_HELPJ	Q921x3 helicobacte
21	27	87.1	773	1 GYRB_HELPJ	P55992 helicobacte
22	27	87.1	1073	1 PVDA_PLAKN	P22545 plasmodium
23	27	87.1	1137	1 A4E1_HUMAN	Q9upm8 homo sapien
24	26	83.9	424	1 COAA_BPFD	P03661 bacterioph
25	26	83.9	424	1 COAA_BPFD	P03662 bacterioph
26	26	83.9	693	1 GUAH_HUMAN	P49915 homo sapien
27	26	83.9	930	1 ATSS_HUMAN	Q9una0 homo sapien
28	26	83.9	930	1 ATSS_MOUSE	Q9r001 mus musculu
29	25	80.6	27	1 CXOT_CONCN	P58916 conus conso
30	25	80.6	179	1 YGJP_ECOLI	P42597 escherichia
31	25	80.6	198	1 NUDC_EMENI	P17624 emericella
32	25	80.6	210	1 SRB2_YEAST	P34162 saccharomyc
33	25	80.6	218	1 COAT_CWVAS	Q66154 cucumber mo

ALIGNMENTS

RESULT 1

ID	CXOC_CONCT	STANDARD;	PRT;	26 AA.
AC	P58919;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Omega-conotoxin CVIC.			
OS	Conus catus (Cat cone).			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;			
OC	Neogastropoda; Conoidea; Conidae; Conus.			
OX	NCBI_TaxID=101291;			
RN	[1]			
RP	SEQUENCE, AND SYNTHESIS.			
RC	TISSUE=Venom;			
RX	PubMed=10938268;			
RA	Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,			
RA	Sharpe R.J., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,			
RA	Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;			
RT	"Novel omega-conotoxins from Conus catus discriminate among neuronal			
RT	calcium channel subtypes."			
RL	J. Biol. Chem. 275:35335-35344(2000).			
CC	-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind			
CC	and block voltage-sensitive calcium channels (VSCC) (By			
CC	similarity). This toxin blocks N-, P-, and Q-type calcium			
CC	channels.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: Expressed by the venom duct.			
CC	-!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE			
CC	FAMILY.			
KW	Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;			
KW	Amidation.			
FT	DISULFID 1 16 BY SIMILARITY.			
FT	DISULFID 8 20 BY SIMILARITY.			
FT	DISULFID 15 26 BY SIMILARITY.			
FT	MOD_RES 26 26 AMIDATION.			
SQ	SEQUENCE 26 AA; 2790 MW; 56EFC382335C4A8B CRC64;			

Query Match 100.0%; Score 31; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.29;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6

|||||

Db 9 SKLMYD 14

RESULT 2

ID	CXOD_CONCT	STANDARD;	PRT;	73 AA.
AC	P58920;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Omega-conotoxin CVID precursor.			
OS	Conus catus (Cat cone).			

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=101291;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 46-72, SYNTHESIS, AND STRUCTURE BY
 RP NMR.
 RC TISSUE=Venom duct, and Venom;
 RX PubMed=10938268;
 RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
 RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
 RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
 RT "Novel omega-conotoxins from *Conus catus* discriminate among neuronal
 RT calcium channel subtypes.";
 RL J. Biol. Chem. 275:35335-35344(2000).
 CC -1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC) (By
 CC similarity). This toxin blocks N-type calcium channels.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 CC FAMILY.
 KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
 KW Analization; Signal. 22 POTENTIAL.
 FT SIGNAL 1 22
 FT PROPEP 23 45
 FT PEPTIDE 46 72 OMEGA-CONOTOXIN CVID.
 FT DISULFID 46 61 BY SIMILARITY.
 FT DISULFID 53 65 BY SIMILARITY.
 FT DISULFID 60 72 BY SIMILARITY.
 FT MOD_RES 72 72 AMIDATION (G-73 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 73 AA; 7748 MW; C4CEBD30C77DAEC3 CRC64;
 Query Match 100.0%; Score 31; DB 1; Length 73;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SKLMYD 6
 Db 54 SKLMYD 59
 RESULT 3
 CXOA_CONNA STANDARD; PRT; 71 AA.
 ID CXOA_CONNA
 AC P05484;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Omega-conotoxin MvIIa precursor (SNX-111) (ziconotide).
 OS *Conus magus* (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OC NCBI_TaxID=6492;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom duct;
 RX PubMed=10938268;
 RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
 RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
 RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
 RT "Novel omega-conotoxins from *Conus catus* discriminate among neuronal
 RT calcium channel subtypes.";
 RL J. Biol. Chem. 275:35335-35344(2000).
 CC [2]
 RN SEQUENCE OF 46-70.
 RP MEDLINE=86070213; PubMed=4071055;
 RA Olivera B.M., Gray W.R., Zeikus R.D., McIntosh J.M., Varga J.,
 RA Rivier J.E., de Santos V., Cruz L.J.;
 RT "Peptide neurotoxins from fish-hunting cone snails.";
 RL Science 230:1338-1343(1985).
 RN [3]
 RP SEQUENCE OF 46-70.
 RP MEDLINE=87299637; PubMed=2441741;

RA Olivera B.M., Cruz L.J., de Santos V., Lecheminant G.W., Griffin D.,
 RA Zeikus R.D., McIntosh J.M., Galyean R., Varga J., Gray W.R.,
 RA Rivier J.E.;
 RT "Neuronal calcium channel antagonists. Discrimination between calcium
 RT channel subtypes using omega-conotoxin from *Conus magus* venom.";
 RL Biochemistry 26:2086-2090(1987).
 RN [4]
 RP DISULFIDE BONDS.
 RX PubMed=8537186;
 RA Chung D., Gaur S., Bell J.R., Ramachandran J., Nadasdi L.;
 RT "Determination of disulfide bridge pattern in omega-conopeptides.";
 RL Int. J. Pept. Protein Res. 46:320-325(1995).
 RN [5]
 RP SYNTHESIS, AND MUTAGENESIS OF LYS-47 AND TYR-58.
 RX PubMed=7826361;
 RA Kim J.I., Takahashi M., Ohtake A., Wakamiya A., Sato K.;
 RT "Tyr13 is essential for the activity of omega-conotoxin MvIIA and
 RT GVIA, specific N-type calcium channel blockers.";
 RL Biochem. Biophys. Res. Commun. 206:449-454(1995).
 RN [6]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95367555; PubMed=7640281;
 RA Kohno T., Kim J.-I., Kobayashi K., Koderia Y., Maeda T., Sato K.;
 RT "Three-dimensional structure in solution of the calcium channel
 RT blocker omega-conotoxin MvIIA.";
 RL Biochemistry 34:10256-10265(1995).
 RN [7]
 RP STRUCTURE BY NMR.
 RX PubMed=7656969;
 RA Basus V.J., Nadasdi L., Ramachandran J., Miljanich G.P.;
 RT "Solution structure of omega-conotoxin MvIIA using 2D NMR
 RT spectroscopy.";
 RL FEBS Lett. 370:163-169(1995).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97070382; PubMed=8913308;
 RA Nielsen K.J., Thomas L., Lewis R.J., Alewood P.F., Craik D.J.;
 RT "A consensus structure for omega-conotoxins with different
 RT selectivities for voltage-sensitive calcium channel subtypes:
 RT comparison of MvIIA, SVIB and SNX-202.";
 RL J. Mol. Biol. 263:297-310(1996).
 RN [9]
 RP STRUCTURE BY NMR.
 RX PubMed=10373375;
 RA Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
 RA Lewis R.J.;
 RT "Structure-activity relationships of omega-conotoxins MvIIA, MvIIC and
 RT 14 loop splice hybrids at N and P/Q-type calcium channels.";
 RL J. Mol. Biol. 289:1405-1421(1999).
 RN [10]
 RP STRUCTURE BY NMR.
 RX PubMed=10747778;
 RA Atkinson R.A., Kieffer B., Dejaegere A., Sirockin F., Lefevre J.-F.;
 RT "Structural and dynamic characterization of omega-conotoxin MvIIA: the
 RT binding loop exhibits slow conformational exchange.";
 RL Biochemistry 39:3908-3919(2000).
 RN [11]
 RP STRUCTURE BY NMR.
 RX MEDLINE=21243158; PubMed=11344322;
 RA Goldenberg D.P., Koehn R.E., Gilbert D.E., Wagner G.;
 RT "Solution structure and backbone dynamics of an omega-conotoxin
 RT precursor.";
 RL Protein Sci. 10:538-550(2001).
 CC -1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC). This toxin
 CC blocks N-type calcium channels.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- PHARMACEUTICAL: Is under clinical trial by Neurex. It blocks acute
 CC pain in patients who no longer obtain relief from opiate drugs. It
 CC is 100 to 1000 times more potent than morphine. By blocking
 CC calcium channels it disables nerves that transmit pain signals.
 CC -1- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE

```

CC FAMILY.
CC -!- DATABASE: NAME=ziconotide Source; NOTE-Web site on ziconotide;
CC WWW="http://dcmnd.com/ziconotide/".
DR PIR: C60133; C60133.
DR PIR: JH0700; JH0700.
DR PDB: IOMG; 03-APR-96.
DR PDB: IMVI; 12-AUG-97.
DR PDB: IDW4; 01-MAR-00.
DR PDB: IDW5; 01-MAR-00.
DR PDB: IPE0; 23-AUG-00.
KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
KW Amidation; Signal; 3D-structure; Pharmaceutical.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 45
FT PEPTIDE 46 70 OMEGA-CONOTOXIN MWIIA.
FT DISULFID 46 61
FT DISULFID 53 65
FT DISULFID 60 70
FT MOD_RES 70 70
FT MUTAGEN 47 47
FT MUTAGEN 58 58
SQ SEQUENCE 71 AA; 7587 MW; E2A32725C81AF31D CRC64;

Query Match 90.3%; Score 28; DB 1; Length 71;
Best Local Similarity 83.3%; Pred. No. 4.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
DB 54 SKLMYD 59

RESULT 4
YE63_CAMJE
ID YE63_CAMJE STANDARD: PRT: 113 AA.
AC Q9PMJ7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein Cj1463.
GN Cj1463.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Kettle J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
CC -!- SIMILARITY: TO H. PYLORI HP0245/JHP0230.
CC -----
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CC -----
CC EMBL; AL139078; CAB73886.1;
CC Hypothetical protein; Complete proteome.
KW SEQUENCE 113 AA; 12670 MW; E33E72713C188C31 CRC64;
SQ SEQUENCE 113 AA; 12670 MW; E33E72713C188C31 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 113;
Best Local Similarity 83.3%; Pred. No. 6.8;

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Matches 5; Conservative 1; Mismatches 0; Indels; 0; Gaps 0;

QY 1 SKLMYD 6
DB 102 SKLMD 107

RESULT 5
SERC_SCHPO
ID SERC_SCHPO STANDARD: PRT: 389 AA.
AC Q10349;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative phosphoserine aminotransferase (EC 2.6.1.52) (PSAT).
GN SPAC1F12.07.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesti D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- CATALYTIC ACTIVITY: O-phospho-L-serine + 2-oxoglutarate = 3-
CC phosphonooxypyruvate + L-glutamate.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
CC EMBL; Z69944; CAA93811.1;
CC HSSP; Q59196; 1B74.
DR InterPro; IPR00192; Aminotransfv.
DR InterPro; IPR003248; Pser_amintransf.
DR Pfam; PF00266; aminotran_5; 1.
DR ProDom; PD001544; Pser_amintransf; 1.
DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
KW Hypothetical protein; Serine biosynthesis; Transferase;

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SIN4_YEAST	STANDARD	PRT	974 AA
ID	SIN4_YEAST		
AC	P32259;		
DT	01-OCT-1993 (Rel. 27, Created)		
DT	01-OCT-1993 (Rel. 27, Last sequence update)		
DT	01-OCT-1996 (Rel. 34, Last annotation update)		
DE	Global transcriptional regulator SIN4.		
GN	SIN4 OR TSF3 OR BEL2 OR GAL22 OR SF5 OR YNL236W OR NII135.		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.		
OX	NCBI_TaxID=4932;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=YM256;		
RX	MEDLINE=93140781; PubMed=8423805;		
RA	Chen S., West R.W. Jr., Johnson S.L., Gans H., Kruger B., Ma J.;		
RT	"TSF3, a global regulatory protein that silences transcription of		
RT	yeast GAL genes, also mediates repression by alpha 2 repressor and is		
RT	identical to SIN4.";		
RT	Mol. Cell. Biol. 13:831-840(1993).		
RN	[2]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=93024394; PubMed=1406639;		
RC	Jiang Y.W., Stillman D.J.;		
RA	"Involvement of the SIN4 global transcriptional regulator in the		
RT	chromatin structure of Saccharomyces cerevisiae.";		
RT	Mol. Cell. Biol. 12:4503-4514(1992).		
RN	[3]		
RN	SEQUENCE FROM N.A.		
RP	Harashima S., Mabuchi H., Ramash R., Hasebe M., Tanaka A., Oshima Y.;		
RC	Submitted (AUG-1992) to the EMBL/GenBank/DBJ databases.		
RA	[4]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=97051596; PubMed=8896273;		
RC	Pandolfo D., de Antoni A., Lanfranchi G., Valle G.;		
RA	"The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open		
RT	reading frames including a novel gene encoding a globin-like		
RT	domain.";		
RT	Yeast 12:1071-1076(1996).		
CC	!- FUNCTION: GLOBAL REGULATORY PROTEIN THAT SILENCES TRANSCRIPTION		
CC	OF GAL AND MATING-TYPE GENES. NEGATIVE REGULATOR OF THE HO		
CC	(HOMOTHALISM) GENE. MAY POTENTIATE TRANSCRIPTIONAL ACTIVATION		
CC	AND REPRESSION BY REGULATING THE ACTIVITY OF THE BASAL		
CC	TRANSCRIPTIONAL APPARATUS. SIN4 MUTATION ALTERS CHROMATIN		
CC	STRUCTURE.		
CC	!- SUBCELLULAR LOCATION: Nuclear.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collabor		
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CC	use by non-profit institutions as long as its content is in no		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/anno		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; M93050; AAA35044.1; -		
DR	EMBL; X64516; CAA45819.1; -		
DR	EMBL; D12918; BAA02302.1; -		
DR	EMBL; Z69381; CAA93362.1; -		
DR	EMBL; Z71512; CAA96140.1; -		
DR	PIR; A4484; A44484;		
DR	PIR; S20132; S20132;		
DR	PIR; A48074; A48074;		
DR	PIR; S41805; S41805;		
DR	TRANSFAC; T01243; -		
DR	SGD; S0005180; SIN4.		
DR	Transcription regulation; Activator; DNA-binding; Repressor;		
KW	Nuclear protein.		
KW	81		
FT	DOMAIN 63		
FT	DOMAIN 889		
FT	DOMAIN 893		
FT	DOMAIN 974 AA; 111296 MW; 2ECF5E4CDC05A8E CRC64;		
SQ	SEQUENCE		


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Query Match          90.3%; Score 28; DB 1; Length 974;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
DB 901 SKLIYD 906

RESULT 8
YCF3_PORPU
ID YCF3_PORPU STANDARD; PRT; 173 AA.
AC P51258;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Photosystem I assembly protein ycf3.
GN YCF3.
OS Porphyra purpurea.
OC Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Porphyra.
OX NCBI_TaxID=2787;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Avonport;
RA Reith M.E., Munholland J.;
RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast genome";
RL Plant Mol. Biol. Rep. 13:333-335(1995).
CC -!- FUNCTION: Seems to be required for the assembly of the photosystem I complex (By similarity).
CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By similarity).
CC -!- SIMILARITY: BELONGS TO THE YCF3 FAMILY.
CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC
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CC
CC EMBL; U38804; AAC08144.1; -
CC DR InterPro: IPR001440; TPR.
CC DR Pfam: PF00515; TPR 3.
CC DR SMART: SM00028; TPR; 3.
CC KW Photosynthesis; Thylakoid; Membrane; Repeat; TPR repeat; Chloroplast.
CC FT REPEAT 35 68 TPR 1.
CC FT REPEAT 72 105 TPR 2.
CC FT REPEAT 120 153 TPR 3.
CC SQ SEQUENCE 173 AA; 20185 MW; A089AFE8DD790BF5 CRC64;

Query Match          87.1%; Score 27; DB 1; Length 173;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
DB 132 SKLMFD 137

RESULT 9
YJBM_ECOLI
ID YJBM_ECOLI STANDARD; PRT; 235 AA.
AC P32694; P76785;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yjbm.
GN YJBM OR B4048.
OS Escherichia coli.

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```

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RA MEDLINE=94089392; PubMed=8265357;
RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA Daniels D.L.;
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes.";
RL Nucleic Acids Res. 21:5408-5417(1993).
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CC
CC EMBL; U00006; AAC43142.1; -
CC DR EMBL; AE000478; AAC77018.1; -
CC DR Ecogene; EGI1931; yjbm.
CC KW Hypothetical protein; Complete proteome.
CC SQ SEQUENCE 235 AA; 26673 MW; A5BB8A1E6F20E0B6 CRC64;

Query Match          87.1%; Score 27; DB 1; Length 235;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
DB 222 SKLIYD 227

RESULT 10
NRTB_SYNY3
ID NRTB_SYNY3 STANDARD; PRT; 275 AA.
AC P73451;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nitrate transport permease protein nrtb.
GN NRTB OR SLL1451.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- FUNCTION: PROBABLY PART OF A HIGH-AFFINITY BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR NITRATE; PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM PERMEASE FAMILY. CYSTW SUBFAMILY.
CC
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DR EMBL; D90906; BAA17491.1; -;
 DR InterPro; IPR000515; BPD_transp.
 DR Pfam; PF00528; BPD_transp; 1.
 DR TIGRFAMs; TIGR01183; ntrB; 1.
 DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; FALSE_NEG.
 KW Transport; Transmembrane; Nitrate assimilation; Complete proteome.
 FT TRANSMEM 25 45 POTENTIAL.
 FT TRANSMEM 89 109 POTENTIAL.
 FT TRANSMEM 147 167 POTENTIAL.
 FT TRANSMEM 189 209 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 FT TRANSMEM 238 258 POTENTIAL.
 SQ SEQUENCE 275 AA; 29720 MW; 47CDB9366185F99E CRC64;

Query Match 87.1%; Score 27; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SKLMDV 6
 Db 110 SKFMYD 115

RESULT 11
 VE2_HP70 STANDARD; PRT; 360 AA.
 AC P50773;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Regulatory protein E2.
 GN E2.
 OS Human papillomavirus type 70.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=39457;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96249586; PubMed=8815087;
 RA Forslund O., Hansson B.G.;
 RT "Human papillomavirus type 70 genome cloned from overlapping PCR
 products: complete nucleotide sequence and genomic organization.";
 RL J. Clin. Microbiol. 34:802-809(1996).
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DR EMBL; U21941; AAC54853.1; -;
 DR HSP; P17383; 1DHM.
 DR InterPro; IPR000427; E2_C.
 DR InterPro; IPR001866; E2_N.
 DR Pfam; PF00508; E2_N; 1.
 DR Pfam; PF00511; E2_C; 1.
 DR ProDom; PD000672; E2_C; 1.
 DR ProDom; PD000678; E2_N; 1.
 SQ SEQUENCE 360 AA; 41519 MW; 2B5A5932AB67AA0 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 360;
 Best Local Similarity 83.3%; Pred. No. 38;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMDV 6
 Db 28 SKLMDV 33

RESULT 12
 SERC_DROME STANDARD; PRT; 364 AA.
 AC Q9VANO;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable phosphoserine aminotransferase (EC 2.6.1.52) (PSAT).
 GN ESTS:39C10S OR CG11899.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Moulton G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclele J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -!- CATALYTIC ACTIVITY: O-phospho-L-serine + 2-oxoglutarate = 3-
 CC phosphonoxypropylate + L-glutamate.
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -!- PATHWAY: REQUIRED BOTH IN MAJOR PHOSPHORYLATED PATHWAY OF SERINE
 CC BIOSYNTHESIS AND IN THE BIOSYNTHESIS OF PYRIDOXINE.
 CC -!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
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DR EMBL; AE003768; AAF56874.1; -.
DR HSP; P23721; 1BJN.
DR FlyBase; FBgn0014427; ESTS:39C10S.
DR InterPro; IPR000192; AminoTransf.
DR InterPro; IPR003248; Pser_amintransf.
DR Pfam; PF00266; aminotran_5; 1.
DR ProDom; PD001544; Pser_amintransf; 1.
DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
KW Serine biosynthesis; Transferase; AminoTransferase;
KW Pyridoxal phosphate.
FT BINDING 194 194 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 364 AA; 39540 MW; DAE4E2F5BD4DB74 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 364;
Best Local Similarity 83.3%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMD 6
DB 269 SKLIYD 274

RESULT 13
SYN_ORYSA STANDARD; PRT; 494 AA.
AC P93422;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
DE (HisRS).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
ON NCBI_TaxID=4530;
RX SEQUENCE FROM N.A.
RA Hagemann T.L., Kwan S.-P.;
RT "The identification and characterization of two promoters and the
complete genomic sequence for the Wiskott-Aldrich syndrome gene.";
RL Biochem. Biophys. Res. Commun. 256:104-109(1999).
CC -!- CATALYTIC ACTIVITY: ATP + L-histidyl-tRNA(His)
diphosphate + L-histidyl-tRNA(His).
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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or send an email to license@isb-sib.ch).
CC
DR EMBL; Z85984; CAB06653.1; -.
DR InterPro; IPR002106; AALRNA_ligaseII.
DR InterPro; IPR004154; HGTP anticodon.
DR InterPro; IPR004516; HisS.
DR InterPro; IPR002314; tRNA-synt_2b.
DR Pfam; PF00587; tRNA-synt_2b; 1.
DR Pfam; PF03129; HGTP-anticodon; 1.
DR TIGRfams; TIGR00442; hisS; 1.
DR PROSITE; PS50862; AA_TRNA_LIGASE-II; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SQ SEQUENCE 494 AA; 55320 MW; 79B8B57604682AB2 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 494;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMD 6
DB 114 SKLIYD 119
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RESULT 14
WASP_HUMAN STANDARD; PRT; 502 AA.
ID P42768; Q9UNJ9; Q9BUI1;
AC P42768; Q9UNJ9; Q9BUI1;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Wiskott-Aldrich syndrome protein (WASP).
GN WAS OR IMD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=94349367; PubMed=8069912;
RA Derry J.M.J., Ochs H.D., Francke U.;
RT "Isolation of a novel gene mutated in Wiskott-Aldrich syndrome.";
RL Cell 78:635-644(1994).
RN [2]
RP ERRATUM.
RX MEDLINE=95094263; PubMed=8001129;
RA Derry J.M.J., Ochs H.D., Francke U.;
RL Cell 79:923-923(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95273432; PubMed=7753869;
RA Kwan S.P., Hagemann T.L., Radtke B.E., Blaese R.M., Rosen F.S.;
RT "Identification of mutations in the Wiskott-Aldrich syndrome gene and
characterization of a polymorphic dinucleotide repeat at DXS6940,
adjacent to the disease gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:4706-4710(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99167346; PubMed=10066431;
RA Hagemann T.L., Kwan S.-P.;
RT "The identification and characterization of two promoters and the
complete genomic sequence for the Wiskott-Aldrich syndrome gene.";
RL Biochem. Biophys. Res. Commun. 256:104-109(1999).
RN [5]
RP SEQUENCE FROM N.A.
RA Blechschmidt K., Nyakatura G., Strom T.M., Drescher B., Menzel U.,
Meindl A., Rosenthal A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP VARIANTS WAS K-31; M-75; P-82; C-86; H-86; C-97; K-133; E-476 AND
H-30 DEL.
RX MEDLINE=96133285; PubMed=8528198;
RA Kolluri R., Shehabeldin A., Peacocke M., Lamhonwah A.-M.,
Teichert-Kuliszewska K., Weissman S.M., Siminovich K.A.;
RT "Identification of WASP mutations in patients with Wiskott-Aldrich
syndrome and isolated thrombocytopenia reveals allelic heterogeneity
at the WAS locus.";
RL Hum. Mol. Genet. 4:1119-1126(1995).
RN [8]
RP VARIANTS WAS P-27; I-48; M-75; L-86; H-86; K-131; C-187 AND K-477.
RX MEDLINE=96133286; PubMed=8528199;
RA Derry J.M.J., Kerns J.A., Weinberg K.I., Ochs H.D., Voipini V.,
Estivill X., Walker A.P., Francke U.;
RT "WASP gene mutations in Wiskott-Aldrich syndrome and X-linked
thrombocytopenia.";
RL Hum. Mol. Genet. 4:1127-1135(1995).
RN [9]
RP VARIANTS WAS VAL-56 AND GLU-236.
RX MEDLINE=95315993; PubMed=7795648;
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DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE histidyl-trNA synthetase (EC 6.1.1.21) (Histidine--trNA ligase)
DE (HRSR).
GN HARS OR HRS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92195807; PubMed=1549469;
RA Raben N., Borriello F., Amin J., Horwitz R., Fraser D., Plotz P.;
RA "Human histidyl-trNA synthetase: recognition of amino acid signature
RT regions in class 2a aminoacyl-trNA synthetases.";
RL Nucleic Acids Res. 20:1075-1081(1992).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=87203366; PubMed=3554142;
RA Tsui F.W.L., Siminovitch L.;
RA "Isolation, structure and expression of mammalian genes for histidyl-
RT trNA synthetase.";
RL Nucleic Acids Res. 15:3349-3367(1987).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Uterus;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE OF 1-30 FROM N.A.
RX MEDLINE=94010309; PubMed=8406012;
RA Tsui H.W., Mok S., de Souza L., Martin A., Tsui F.W.L.;
RA "Transcriptional analyses of the gene region that encodes human
RT histidyl-trNA synthetase: identification of a novel bidirectional
RT regulatory element.";
RL Gene 131:201-208(1993).
RN [5]
RN SEQUENCE OF 1-30 FROM N.A.
RX MEDLINE=95275311; PubMed=7755634;
RA O'Hanlon T.P., Raben N., Miller F.W.;
RA "A novel gene oriented in a head-to-head configuration with the human
RT histidyl-trNA synthetase (HRS) gene encodes an mRNA that predicts a
RT polypeptide homologous to HRS.";
RL Biochem. Biophys. Res. Commun. 210:556-566(1995).
CC -! CATALYTIC ACTIVITY: ATP + L-histidine + trNA(His) = AMP +
CC diphosphate + L-histidyl-trNA(His).
CC -! SUBCELLULAR LOCATION: Cytoplasmic.
CC -! TISSUE SPECIFICITY: BRAIN, HEART, LIVER AND KIDNEY.
CC -! SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -! SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.
CC -! CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
CC FRAMESHIFTS AND OTHER SEQUENCING ERRORS.
CC -----
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CC -----
DR EMBL; Z11518; CAA77607.1; -
DR EMBL; X05345; CAA28956.1; ALT_FRAME.
DR EMBL; BC011807; AAH11807.1; -
DR EMBL; M96646; AA586668.1; -
DR EMBL; U18936; AA73973.1; -
DR PIR; B27516; SYHOHT.
DR PIR; S18985; S18985.
DR Genew; HGNC:4816; HARS.
DR MIM; 142810; -
DR InterPro; IPR002106; AALRNA_ligaseII.
DR InterPro; IPR004154; HGTP_anticonodon.
DR InterPro; IPR004516; Hiss.

DR InterPro; IPR000738; WHEP-TRS.
DR InterPro; IPR002314; trNA-synt_2b.
DR Pfam; PF00458; WHEP-TRS; 1.
DR Pfam; PF00587; trNA-synt_2b; 1.
DR Pfam; PF03129; HGTP_anticonodon; 1.
DR TIGRFAMs; TIGR00442; hirs; 1.
DR PROSITE; PS00862; AA_TRNA_LIGASE_II; 1.
DR PROSITE; PS00762; WHEP-TRS; 1.
KW Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT DOMAIN 14 59 WHEP-TRS.
SQ SEQUENCE 509 AA; 57410 MW; 65D8BB71CE79B1FF CRC64;

Query Match 87.1%; Score 27; DB 1; Length 509;
Best Local Similarity 83.3%; Pred. No. 55;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
Db 111 SKLIYD 116

Search completed: February 26, 2003, 08:37:19
Job time : 4.92308 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:32:54 ; Search time 5.53846 Seconds
(without alignments)
104.146 Million cell updates/sec

Title: US-09-673-490B-2

Perfect score: 31

Sequence: 1 SKLMD 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PTR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	28	90.3	25	2 JH0700	omega-conotoxin MV
2	28	90.3	113	2 F81292	hypothetical prote
3	28	90.3	389	2 S67450	probable phospho
4	28	90.3	460	2 JQ1275	RAD57 protein - ye
5	28	90.3	722	2 T00049	hemocyte protein A
6	28	90.3	927	2 B82075	sensor histidine k
7	28	90.3	974	2 A44484	transcriptional regu
8	27	87.1	108	2 T17826	hypothetical prote
9	27	87.1	154	2 T30372	hypothetical prote
10	27	87.1	173	2 S73179	hypothetical prote
11	27	87.1	235	2 G63212	hypothetical 26.7k
12	27	87.1	250	2 E89827	conserved hypothet
13	27	87.1	275	2 S77388	nitrate transport
14	27	87.1	282	2 T52457	heme oxygenase (de
15	27	87.1	285	2 B96719	probable heme oxyg
16	27	87.1	318	2 B86098	hypothetical prote
17	27	87.1	322	2 AF1830	ATP-binding protei
18	27	87.1	384	2 B86660	amino acid amidohy
19	27	87.1	402	2 C97132	hypothetical prote
20	27	87.1	459	2 JC6520	interferon regulat
21	27	87.1	494	2 T03774	probable histidine
22	27	87.1	502	2 A55197	Wiskott-Aldrich sy
23	27	87.1	509	1 SYH021	histidine-tRNA lig
24	27	87.1	509	1 JCS223	histidine-tRNA lig
25	27	87.1	538	1 T40151	histidine-tRNA lig
26	27	87.1	540	2 T19097	hypothetical prote
27	27	87.1	562	2 S76807	hypothetical prote
28	27	87.1	566	2 S75233	ABC transporter sl
29	27	87.1	773	2 E64582	DNA gyrase, sub B

30 27 87.1 773 2 B71931 DNA gyrase chain B
31 27 87.1 859 2 F81863 clpB protein NMA16
32 27 87.1 859 2 F81078 clpB protein NMB14
33 27 87.1 1757 2 T14318 ubiquitin-protein
34 27 87.1 1832 2 T31113 mucin-like glycopr
35 26 83.9 156 2 T07174 tuberin-like glycopr
36 26 83.9 201 2 C82908 tuberin-like glycopr
37 26 83.9 424 1 Z3BPF0 coat protein A pre
38 26 83.9 424 1 Z3BPM3 coat protein A pre
39 26 83.9 424 1 Z3BPF1 coat protein A pre
40 26 83.9 478 2 D97266 glutamyl-tRNA^{Gln} a
41 26 83.9 501 2 T25317 hypothetical prote
42 26 83.9 596 2 G97133 phage terminase-11
43 26 83.9 693 2 A54847 GMP synthase (glut
44 26 83.9 809 2 E71660 hypothetical prote
45 26 83.9 929 2 T32492 hypothetical prote

ALIGNMENTS

RESULT 1

JH0700

omega-conotoxin MVIIA [validated] - cone shell (Conus magus)

C:Species: Conus magus (magus cone)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Sep-2000

C:Accession: JH0700; C60133; A34115

R:Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J

Neuron 9, 69-77, 1992

A:Title: A new conus peptide ligand for mammalian presynaptic Ca²⁺ channels.

A:Reference number: JH0699; MUID:92337922; PMID:1352986

A:Accession: JH0700

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-25 <HLL>

R:Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de S

Science 230, 1338-1343, 1985

A:Title: Peptide neurotoxins from fish-hunting cone snails.

A:Reference number: A43620; MUID:86070213; PMID:4071055

A:Accession: C60133

A:Molecule type: protein

A:Residues: 1-25 <OLI>

R:Olivera, B.M.; Cruz, L.J.; de Santos, V.; Lecheminant, G.W.; Griffin, D.; Zeikus, J

Biochemistry 26, 2086-2090, 1987

A:Title: Neuronal calcium channel antagonists. Discrimination between calcium channel

A:Reference number: A34115; MUID:87299637; PMID:2441741

A:Contents: annotation

R:Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.

submitted to the Brookhaven Protein Data Bank, August 1996

A:Reference number: A67648; PDB:1MVI

A:Contents: annotation; conformation by (1)H-NMR, residues 1-25

R:Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.

J. Mol. Biol. 263, 297-310, 1996

A:Title: A consensus structure for omega-conotoxins with different selectivities for

A:Reference number: A58619; MUID:97070382; PMID:8913308

A:Contents: annotation; conformation by (1)H-NMR

R:Kohn, T.; Kim, J.I.; Kobayashi, K.; Kodera, Y.; Maeda, T.; Sato, K.

submitted to the Brookhaven Protein Data Bank, April 1995

A:Reference number: A66296; PDB:1OMG

A:Contents: annotation; conformation by (1)H-NMR, residues 1-25

R:Kohn, T.; Kim, J.I.; Kobayashi, K.; Kodera, Y.; Maeda, T.; Sato, K.

Biochemistry 34, 10256-10265, 1995

A:Title: Three-dimensional structure in solution of the calcium channel blocker omeg

A:Reference number: A58627; MUID:95367555; PMID:7640281

A:Contents: annotation; conformation by (1)H-NMR

C:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel

F:1-16, 8-20, 15-25/Disulfide bonds: #status predicted

F:25/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 90.3%; Score 28; DB 2; Length 25;

Best Local Similarity 83.3%; Pred. No. 2.2;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
I:||||
Db 9 SRLMYD 14

RESULT 2
F81292
hypothetical protein Cj1463 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C:Accession: F81292
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chillingworth, N.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrett, T.; et al. 2000
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervirulence
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: F81292
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-113 <PAR>
A:Cross-references: GB:AL111168; GB:AL139078; NID:g6968723; PIDN:CA873886.1; PID:g6968892
A:Experimental source: serotype O2, strain NCTC 11168
A:Genetics:
C:Superfamily: Helicobacter pylori hypothetical protein HP0245

Query Match 90.3%; Score 28; DB 2; Length 113;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
I:||||
Db 102 SKLLYD 107

RESULT 3
S67450
probable phosphoserine aminotransferase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C:Accession: T38065; S67450
R:McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z21766
A:Accession: T38065
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-389 <MC2>
A:Cross-references: EMBL:Z69944; NID:g1217974; PIDN:CAA93811.1; PID:g1217981; GSPDB:GN000000000
A:Experimental source: strain 972h-; cosmid c1f12
A:Genetics:
C:Superfamily: phosphoserine aminotransferase

Query Match 90.3%; Score 28; DB 2; Length 389;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
I:||||
Db 299 SKLLYD 304

RESULT 4
JQ1275
RAD57 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YD8119.10; protein YDR004W
C:Species: Saccharomyces cerevisiae
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 02-Feb-2001
C:Accession: JQ1275; S50985
R:Kans, J.A.; Mortimer, R.K.

Gene 105, 139-140, 1991
A:Title: Nucleotide sequence of the RAD57 gene of Saccharomyces cerevisiae.
A:Reference number: JQ1275; MUID:92039012; PMID:1937004
A:Accession: JQ1275
A:Molecule type: DNA
A:Residues: 1-460 <KAN>
A:Cross-references: GB:M65061; NID:g172344; PIDN:AAA34950.1; PID:g172345
R:Murphy, L.; Richards, C.; Gentles, S.; Harris, D.
submitted to the EMBL Data Library, January 1995
A:Reference number: S50976
A:Accession: S50985
A:Molecule type: DNA
A:Residues: 1-460 <MUR>
A:Cross-references: EMBL:Z48008; NID:g642799; PID:g642809; MIPS:YDR004W
C:Comment: This protein participates in the repair of radiation-induced damage to DNA
C:Genetics:
A:Gene: SGD:RAD57
A:Cross-references: SGD:S0002411; MIPS:YDR004W
A:Map position: 4R
C:Keywords: nucleotide binding; nucleus; P-loop
F:125-132/Region: nucleotide-binding motif A (P-loop)
F:221-226/Region: nucleotide-binding motif B

Query Match 90.3%; Score 28; DB 2; Length 460;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
I:||||
Db 23 SKLLYD 28

RESULT 5
T00049
hemocyte protein A74 precursor - sea squirt (Halocynthia roretzi)
N:Alternate names: A74 antigen protein
C:Species: Halocynthia roretzi
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 20-Jun-2000
C:Accession: T00049; S63496
R:Takahashi, H.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z14081
A:Accession: T00049
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-722 <TAK>
A:Cross-references: EMBL:AB007512
R:Takahashi, H.; Azumi, K.; Yokosawa, H.
Eur. J. Biochem. 233, 778-783, 1995

A:Title: A novel membrane glycoprotein involved in ascidian hemocyte aggregation and
A:Reference number: S63496; MUID:96085141; PMID:8521842
A:Accession: S63496
A:Molecule type: protein
A:Residues: 20-23, X', 25-28, X', 30-37 <TA2>
C:Superfamily: sea squirt hemocyte protein A74
C:Keywords: glycoprotein; hemolymph; surface antigen
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-722/Product: hemocyte protein A74 #status experimental <MAT>
F:29/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:173,238,257,270,301,323,402,418,465,560,570,625/Binding site: carbohydrate (Asn) (c

Query Match 90.3%; Score 28; DB 2; Length 722;
Best Local Similarity 83.3%; Pred. No. 86;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
I:||||
Db 420 SKLLYD 425

RESULT 6
B82075
sensor histidine kinase/response regulator VC2453 [imported] - Vibrio cholerae (strain

C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: B82075
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
 I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: B82075
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-927 <HEI>
 A:Cross-references: GB:AE004315; GB:AE003852; NID:g9657024; PIDN:AAF95595.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC2453
 A:Map position: 1
 C:Superfamily: sensor-regulator protein barA; response regulator homology

Query Match 90.3%; Score 28; DB 2; Length 927;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
 I:|||||
 Db 194 SRLMYD 199

RESULT 7
 A44484
 transcription regulator SIN4 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: BEL2 protein; protein N1135; protein YNL236W
 C:Species: Saccharomyces cerevisiae
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
 C:Accession: A44484; S41805; A48074; S63202; S67362; S72080; S20132
 R:Jiang, Y.W.; Stillman, D.J.
 Mol. Cell. Biol. 12, 4503-4514, 1992
 A>Title: Involvement of the SIN4 global transcriptional regulator in the chromatin struc
 A:Reference number: A44484; MUID:93024394; PMID:1406639
 A:Accession: A44484
 A:Molecule type: DNA
 A:Residues: 1-974 <JIA>
 A:Cross-references: EMBL:M93050; NID:g172601; PIDN:AAA35044.1; PID:g172602
 A:Note: sequence extracted from NCBI backbone (NCBIP:114172)
 R:Harashima, S.; Mabuchi, H.; Ramash, R.; Hasebe, M.; Tanaka, A.; Oshima, Y.
 submitted to the EMBL Data Library, November 1992
 A:Description: BEL2/SIN4/TSF3 encodes a position-dependent general repressor of a divers
 A:Reference number: S41805
 A:Accession: S41805
 A:Molecule type: DNA
 A:Residues: 1-974 <HAR>
 A:Cross-references: EMBL:D12018; NID:g218405; PID:g218406
 R:Chen, S.; West Jr., R.W.; Johnson, S.L.; Gans, H.; Kruger, B.; Ma, J.
 Mol. Cell. Biol. 13, 831-840, 1993
 A>Title: TSF3, a global regulatory protein that silences transcription of yeast GAL gene
 A:Reference number: A48074; MUID:93140781; PMID:8423805
 A:Accession: A48074
 A:Molecule type: DNA
 A:Residues: 1-974 <CHE>
 A:Cross-references: EMBL:X64516; NID:g4680; PIDN:CAA45819.1; PID:g4681
 A:Note: sequence extracted from NCBI backbone (NCBIN:123362, NCBIP:123363)
 R:Pandolfo, D.; De Antoni, A.; Lanfranchi, G.; Valle, G.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63188
 A:Accession: S63202
 A:Molecule type: DNA
 A:Residues: 1-974 <PAN>
 A:Cross-references: EMBL:Z71512; NID:g1302264; PID:g1302265; MIPS:YNL236W
 A:Experimental source: strain S288C
 R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.
 submitted to the EMBL Data Library, February 1996
 A:Description: DNA sequence of cosmid 14-5 from chromosome XIV.

A:Reference number: S67355
 A:Accession: S67362
 A:Molecule type: DNA
 A:Residues: 1-974 <PAN>
 A:Cross-references: EMBL:Z69381; NID:g1183970; PID:g1183978
 R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.
 Yeast 12, 1071-1076, 1996
 A>Title: The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open reading
 A:Reference number: S72073; MUID:97051596; PMID:8896273
 A:Accession: S72080
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-974 <PAF>
 A:Cross-references: EMBL:Z69381; NID:g1183970; PIDN:CAA93362.1; PID:g1183978
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Genetics:
 A:Gene: SGD:SIN4; TFS3; BEL2; GAL22; SSN4; SDI3
 A:Cross-references: MIPS:YNL236W; SGD:S0005180
 A:Map position: 14L
 C:Function:
 A:Description: transcription regulation
 A:Note: involved in transcriptional silencing mediated by the alpha-2 repressor
 C:Superfamily: Saccharomyces cerevisiae transcription regulator SIN4
 C:Keywords: DNA binding; nucleus; transcription regulation

Query Match 90.3%; Score 28; DB 2; Length 974;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
 I:|||||
 Db 901 SKLLYD 906

RESULT 8
 T17826
 hypothetical protein a327R - Chlorella virus PBCV-1
 C:Species: Chlorella virus PBCV-1
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T17826
 R:Graves, M.V.; Van Etten, J.L.
 submitted to the EMBL Data Library, May 1999
 A:Reference number: Z18806
 A:Accession: T17826
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-108 <GRA>
 A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96695.1
 A:Experimental source: specific host Chlorella strain NC64A
 C:Genetics:
 A:Note: a327R
 C:Superfamily: Chlorella virus PBCV-1 hypothetical protein a327R

Query Match 87.1%; Score 27; DB 2; Length 108;
 Best Local Similarity 83.3%; Pred. No. 19;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLMYD 6
 I:|||||
 Db 52 SKPMYD 57

RESULT 9
 T30372
 hypothetical protein ORF25 - Lymantria dispar nuclear polyhedrosis virus
 C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T30372
 R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; R
 Virology 253, 17-34, 1999
 A>Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria
 A:Reference number: Z20836; MUID:99124785; PMID:9887315
 A:Accession: T30372

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-154 <KUZ>
 A:Cross-references: EMBL:AF081810; NID:g3822234; PIDN:AAC70210.1; PID:g3822259
 C:Superfamily: Lymantria dispar nuclear polydrosis virus hypothetical protein ORF25

Query Match 87.1%; Score 27; DB 2; Length 154;
 Best Local Similarity 83.3%; Pred. No. 28;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
 |||||
 Db 114 SKLMYD 119

RESULT 10

S73179
 hypothetical protein 3 - red alga (Porphyra purpurea) chloroplast
 C:Species: chloroplast Porphyra purpurea
 C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 21-Jan-2000
 C:Accession: S73179
 R:Reith, M.; Munnolland, J.
 Plant Mol. Biol. Rep. 13, 333-335, 1995
 A:Title: Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.
 A:Reference number: S73108
 A:Accession: S73179
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-173 <REI>
 A:Cross-references: EMBL:U38804; NID:g1276652; PID:g1276724
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
 C:Genetics:
 A:Gene: ycf3
 A:Genome: chloroplast
 C:Superfamily: chloroplast conserved hypothetical protein 167; tetratricopeptide repeat
 C:Keywords: chloroplast
 F:35-68/Domain: tetratricopeptide repeat homology <TTR>

Query Match 87.1%; Score 27; DB 2; Length 173;
 Best Local Similarity 83.3%; Pred. No. 32;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
 |||||
 Db 132 SKLMYD 137

RESULT 11

G65212
 hypothetical 26.7K protein b4048 - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 C:Accession: G65212
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: G65212
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-235 <BLAT>
 A:Cross-references: GB:AE000478; GB:U00096; NID:g2367339; PIDN:AAC77018.1; PID:g1790482;
 A:Experimental source: strain K-12, substrain W61655
 C:Genetics:
 A:Gene: yjbm
 C:Superfamily: Escherichia coli hypothetical 26.7K protein b4048

Query Match 87.1%; Score 27; DB 2; Length 235;
 Best Local Similarity 83.3%; Pred. No. 45;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
 |||||
 Db 132 SKLMYD 137

Db 222 SKLIVD 227
 |||||

RESULT 12

E89827
 conserved hypothetical protein SA0544 [Imported] - Staphylococcus aureus (strain N315
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: E89827
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O-
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: E89827
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-250 <KUR>
 A:Cross-references: GB:BA000018; PID:g13700479; PIDN:BA041776.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SA0544

Query Match 87.1%; Score 27; DB 2; Length 250;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KLMYD 6
 |||||
 Db 167 KLMYD 171

RESULT 13

S77388
 nitrate transport protein nrtB-2 - Synechocystis sp. (strain PCC 6803)
 N:Alternate names: protein sl11451
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C:Accession: S77388
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
 O.; Kane, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas-
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys-
 S.

A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S77388
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-275 <KAN>
 A:Cross-references: EMBL:D90906; GB:AB001339; NID:g1552492; PIDN:BA017491.1; PID:g165
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Gene: nrtB-2
 C:Superfamily: Synechococcus nitrate transport protein nrtB
 C:Keywords: nitrate transport

Query Match 87.1%; Score 27; DB 2; Length 275;
 Best Local Similarity 83.3%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SKLMYD 6
 |||||
 Db 110 SKLMYD 115

RESULT 14

T52457
 heme oxygenase (decyclizing) (EC 1.14.99.3) precursor, chloroplast [validated] - Arab
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 16-Feb-2001

C:Accession: T52457; D84663
 R:Muramoto, T.; Kohchi, T.; Yokota, A.; Hwang, I.; Goodman, H.M.
 Plant Cell 11, 335-348, 1999
 A:Title: The Arabidopsis photomorphogenic mutant hyl is deficient in phytochrome chromophore
 A:Reference number: 226080; MUID:99172050; PMID:10072395

A:Accession: T52457
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-282 <MUR>
 A:Cross-references: EMBL:AB021858; PIDN:BAA77759.1
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: D84663
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-282 <STO>
 A:Cross-references: GB:AE002093; NID:g4883666; PIDN:AAB95301.2; GSPDB:GN00139

C:Genetics:
 A:Gene: HYL; At2g26670; T9J22.18
 A:Map position: 2
 C:Function:
 A:Description: EC 1.14.99.3 [validated, MUID:99172050]; catalyzes the oxygenation of hem
 C:Keywords: chloroplast; oxidoreductase
 F:1-55/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F:56-282/Product: heme oxygenase #status predicted <NAI>

Query Match 87.1%; Score 27; DB 2; Length 282;
 Best Local Similarity 83.3%; Pred. No. 55;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
 DB 123 SKLVD 128

RESULT 15

B96719
 Probable heme oxygenase T6C23.8 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: B96719
 R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96719
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-285 <STO>
 A:Cross-references: GB:AE005173; NID:g6665544; PIDN:AAF22913.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: T6C23.8
 A:Map position: 1

Query Match 87.1%; Score 27; DB 2; Length 285;
 Best Local Similarity 83.3%; Pred. No. 56;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLMYD 6
 DB 126 SKLVD 131

1

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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:32:19 ; Search time 20.9231 Seconds
(without alignments)
59.087 Million cell updates/sec

Title: US-09-673-490B-1
Perfect score: 30
Sequence: 1 SGTVGR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	91	2 Q06656	Q06656 streptomyces
2	30	100.0	204	12 Q82135	Q82135 gallid herp
3	30	100.0	206	17 Q27094	Q27094 methanobact
4	30	100.0	358	16 Q9RCF4	Q9rcf4 vibrio chol
5	30	100.0	640	10 Q94C10	Q94c10 arabidopsis
6	30	100.0	711	16 P96855	P96855 mycobacteri
7	30	100.0	1249	5 Q9VF33	Q9vf33 drosophila
8	30	100.0	1249	5 Q97043	Q97043 drosophila
9	30	100.0	2026	5 Q8WT29	Q8wt29 leishmania
10	29	96.7	119	2 Q9ZIK7	Q9zik7 helicobacte
11	29	96.7	119	5 Q9VYP3	Q9vyp3 drosophila
12	29	96.7	201	16 Q8XU62	Q8xu62 ralstonia s
13	29	96.7	612	17 Q8TUH0	Q8tuh0 methanosarc
14	29	96.7	829	10 Q8RVQ5	Q8rvq5 arabidopsis
15	29	96.7	863	10 Q94CK5	Q94ck5 arabidopsis
16	27	90.0	63	15 Q85731	Q85731 rous sarcom

17	27	90.0	98	11 Q9JKZ9	Q9jkz9 mus musculus
18	27	90.0	109	4 Q16164	Q16164 homo sapien
19	27	90.0	131	4 Q8TCS3	Q8tcs3 homo sapien
20	27	90.0	136	4 Q96TP6	Q96tp6 homo sapien
21	27	90.0	138	17 Q58962	Q58962 pyrococcus
22	27	90.0	140	17 Q9Y902	Q9y902 aeropyrum p
23	27	90.0	141	16 Q9PEW4	Q9pew4 xylella fas
24	27	90.0	142	4 Q95098	Q95098 homo sapien
25	27	90.0	146	10 Q8W009	Q8w009 hordeum vul
26	27	90.0	189	2 Q48619	Q48619 lactococcus
27	27	90.0	211	4 Q96PJ7	Q96pj7 homo sapien
28	27	90.0	256	17 Q26823	Q26823 methanobact
29	27	90.0	263	11 Q9CUV1	Q9cuv1 mus musculus
30	27	90.0	293	4 Q9BTP0	Q9btp0 homo sapien
31	27	90.0	296	5 Q9VTQ0	Q9vtq0 drosophila
32	27	90.0	309	4 Q9G9F4	Q9g9f4 homo sapien
33	27	90.0	316	5 Q8WPS7	Q8wps7 trypanosoma
34	27	90.0	318	2 Q9L9G1	Q9l9g1 streptomyce
35	27	90.0	327	5 Q9TXJ9	Q9txj9 caenorhabdi
36	27	90.0	328	16 Q9HYJ6	Q9hyj6 pseudomonas
37	27	90.0	334	17 Q8U1Z7	Q8u1z7 pyrococcus
38	27	90.0	378	16 Q9CIE2	Q9cie2 lactococcus
39	27	90.0	388	16 Q9X85	Q9x85 staphylococ
40	27	90.0	392	4 Q9NZT6	Q9nzt6 homo sapien
41	27	90.0	395	12 Q99BH4	Q99bh4 newcastle d
42	27	90.0	431	4 Q9C0B3	Q9c0b3 homo sapien
43	27	90.0	433	10 Q9FFK4	Q9ffk4 arabidopsis
44	27	90.0	439	17 Q9HHU0	Q9hhj0 halobacteri
45	27	90.0	441	2 Q9S1G0	Q9s1g0 pseudomonas

ALIGNMENTS

RESULT 1

Q06656 PRELIMINARY; PRT; 91 AA.
 ID Q06656;
 AC Q06656;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE DD-peptidase /penicillin-binding protein (Fragment).
 GN DAC.
 OS Streptomyces sp. R61.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=31952;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91080851; PubMed=2175384;
 RA Piron-Fraipont C., Lenzini M.V., Dusart J., Ghuyesen J.;
 RT "Transcriptional analysis of the DD-peptidase/penicillin-binding
 RT protein-encoding dac gene of Streptomyces R61: Use of the promoter and
 RT signal sequences in a secretion vector.";
 RL Mol. Gen. Genet. 223:114-120(1990).
 DR EMBL; X55810; CAB97254.1; -;
 DR HSSP; PI5555; 3PTE.
 FT NON_TER 91
 SQ SEQUENCE 91 AA; 9018 MW; 53583903B4058E35 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
 |||||
 Db 3 SGTVGR 8

RESULT 2

Q82135 PRELIMINARY; PRT; 204 AA.
 ID Q82135
 AC Q82135;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNA binding protien.
OS Gallid herpesvirus 3.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=35250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=281MI/1;
RX MEDLINE=93383373; PubMed=9396799;
RA Camp H.S., Silva R.F., Coussens P.M.;
RT "Defective Marek's disease virus contains a gene encoding a potential
RT nuclear DNA binding protein and a HSV a-like sequence.";
RL Virology 196:484-495(1993).
DR EMBL; L10087; AAA46121.1; -
KW DNA-binding.
SQ SEQUENCE 204 AA; 22305 MW; B519526625681689 CRC64;
Query Match 100.0%; Score 30; DB 12; Length 204;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 139 SGTGVR 144
1 SGTGVR 6
|||||
139 SGTGVR 144

RESULT 3
ID 027094 PRELIMINARY; PRT; 205 AA.
AC 027094;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Conserved protein.
GN MTH1013.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Olu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AE000874; AAB85509.1; -
KW Complete proteome.
SQ SEQUENCE 206 AA; 22308 MW; B32FDAE9083B44C5 CRC64;
Query Match 100.0%; Score 30; DB 17; Length 206;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SGTGVR 6
|||||
Db 21 SGTGVR 26

RESULT 4
ID 09RCF4 PRELIMINARY; PRT; 358 AA.
AC 09RCF4;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytoplasmic membrane permease (Ferric vibriobactin ABC transporter,
DE permease protein).
GN VIUG OR VC0778.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LOU15 (EL TOR);
RX MEDLINE=98037504; PubMed=9371453;
RA Wyckoff E.E., Stoeber J.A., Reed K.E., Payne S.M.;
RT "Cloning of a vibrio cholerae vibriobactin gene cluster:
RT identification of genes required for early steps in siderophore
RT biosynthesis.";
RL J. Bacteriol. 179:7055-7062(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LOU15 (EL TOR);
RX MEDLINE=20069642; PubMed=10601218;
RA Wyckoff E.E., Valle A.M., Smith S.L., Payne S.M.;
RT "A multifunctional ATP-binding cassette transporter system from vibrio
RT cholerae transports vibriobactin and enterobactin.";
RL J. Bacteriol. 181:7588-7596(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; U52150; AAD48882.1; -
DR EMBL; AE004163; AAF93943.1; -
DR TIGR; VC0778; -
DR InterPro; IPR000522; FeccCD.
DR Pfam; PF01032; FeccD; 1.
KW Complete proteome.
SQ SEQUENCE 358 AA; 37472 MW; 2B3090FCEFF5ABCD CRC64;
Query Match 100.0%; Score 30; DB 16; Length 358;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SGTGVR 6
|||||
Db 167 SGTGVR 172

RESULT 5
Q94C10 PRELIMINARY; PRT; 640 AA.
ID Q94C10
AC Q94C10;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE AT5g51070/K3K7.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shinn P.,

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RA Tracy S.E., Banh J., Bowser L., Carninci P., Chung M.K.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
RA Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY037264; AAK59865.1;
DR InterPro: IPR003959; AAA_Atpase_cent.
DR InterPro: IPR001270; Chaprinin_c1pA/B.
DR InterPro: IPR004176; Clp_N.
DR Pfam: PF00004; AAA; 1.
DR Pfam: PF02861; Clp_N; 2.
DR PROSITE: PS00870; CLPAB_1; UNKNOWN.1
SQ SEQUENCE 640 AA; 69611 MW; 4C477ECA608E84BB CRC64;
Query Match 100.0%; Score 30; DB 10; Length 640;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGTVGR 6
Db 395 SGTVGR 400
|||||
RESULT 6
P96855 PRELIMINARY; PRT; 711 AA.
ID P96855;
AC P96855;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 74.5 kDa protein (Acyl-CoA dehydrogenase, putative).
GN FAD34 OR RV3573C OR MT3678 OR MTCY06G11.20C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
[1]
SEQUENCE FROM N.A.
RP STRAIN=H37RV;
RC MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
[2]
SEQUENCE FROM N.A.
RP STRAIN=CDC 1551 / OSHKOSH;
RC Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z92774; CAB07147.1;
DR EMBL: AE007169; AAK48037.1;
DR TIGR: MT3678;
DR Tuberculist; RV3573C;
DR InterPro: IPR001552; Acyl-CoA_dh.
DR Pfam: PF00441; Acyl-CoA_dh; 2.
DR Pfam: PF02770; Acyl-CoA_dh_M; 1.

DR Pfam: PF02771; Acyl-CoA_dh_N; 1.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 557 557 F -> I (IN REF. 2).
FT CONFLICT 630 630 R -> W (IN REF. 2).
SQ SEQUENCE 711 AA; 74577 MW; 52B632900EFE196D CRC64;
Query Match 100.0%; Score 30; DB 16; Length 711;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGTVGR 6
Db 139 SGTVGR 144
|||||
RESULT 7
Q9VFF33 PRELIMINARY; PRT; 1249 AA.
ID Q9VFF33;
AC Q9VFF33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Alpha-Man-IIB protein.
GN ALPHA-MAN-IIB OR CG4606.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Cocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gall R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Rابلlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003710; AAF5528.2;
DR FlyBase; FBgn0026616; alpha-Man-IIB.

DR InterPro: IPR001992; Bact_secr_systII.
 DR InterPro: IPR000602; Glyco_hydro_38.
 DR Pfam: PF01074; Glyco_hydro_38; 1.
 DR PROSITE: PS00874; T2SP_F; UNKNOWN_1.
 SQ SEQUENCE 1249 AA; 141917 MW; 03F1A3F15300DD3F CRC64;

Query Match 100.0%; Score 30; DB 5; Length 1249;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTGVR 6
 |||||
 Db 732 SGTGVR 737

RESULT 8

ID O97043 PRELIMINARY; PRT: 1249 AA.
 AC O97043;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Alpha-mannosidase.
 DE ALPHA-MAN-IIIB OR GAD#24/1 OR CG4606.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lukacsovich T., Asztalos Z., Awano W., Yamamoto D.;
 RT "New alpha-mannosidase gene from *Drosophila melanogaster*.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB018079; BAA75817.1;
 DR FlyBase: FBgn0026616; alpha-Man-IIIB.
 DR InterPro: IPR001992; Bact_secr_systII.
 DR InterPro: IPR000602; Glyco_hydro_38.
 DR Pfam: PF01074; Glyco_hydro_38; 1.
 DR PROSITE: PS00874; T2SP_F; UNKNOWN_1.
 SQ SEQUENCE 1249 AA; 141856 MW; F2E5F6A14754CC3E CRC64;

Query Match 100.0%; Score 30; DB 5; Length 1249;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTGVR 6
 |||||
 Db 732 SGTGVR 737

RESULT 9

ID O8WT29 PRELIMINARY; PRT: 2026 AA.
 AC O8WT29;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Possible cell wall surface anchor family protein.
 GN L7069.04.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Bianchetti G., Ciarloni L., Tosato V., Bruschi C.V., Ivens A.C.,
 RA Quail M., Rajandream M.A., Barrell B.G.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RX MEDLINE=98146435; PubMed=9477341;

RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the *Leishmania* major Friedlin genome.";
 RL Genome Res. 8:135-145(1998).
 DR EMBL: AL605486; CAC69156.2;
 DR InterPro: IPR000104; Antifreeze_1.
 DR InterPro: IPR001950; TIF_SOIL.
 DR PRINTS: PR00308; ANTIFREEZE1.
 DR PROSITE: PS01118; SUIL_1; UNKNOWN_1.
 SQ SEQUENCE 2026 AA; 212781 MW; 95196B92206BC4D3 CRC64;

Query Match 100.0%; Score 30; DB 5; Length 2026;
 Best Local Similarity 100.0%; Pred. No. 9.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTGVR 6
 |||||
 Db 451 SGTGVR 456

RESULT 10

ID O9ZIK7 PRELIMINARY; PRT: 119 AA.
 AC O9ZIK7;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Type I restriction enzyme EcoRI specificity protein homolog (Fragment).
 DE Helicobacter pylori (Campylobacter pylori).
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-J166;
 RA MEDLINE=99007275; PubMed=9789049;
 RA Akopyants N.S., Fradkov A., Diatchenko L., Hill J.E., Siebert P.D.,
 RA Lukyanov S.A., Sverdlov E.D., Berg D.E.;
 RT "PCR-based subtractive hybridization and differences in gene content among strains of *Helicobacter pylori*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:13108-13113(1998).
 DR EMBL: AF025968; AAC69256.1;
 DR REBASE: 4017; S.Hpy166BP.
 DR InterPro: IPR000055; Methylase_S.
 DR Pfam: PF01420; Methylase_S; 1.
 FT NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13744 MW; DD0D2BFBEF908024 CRC64;

Query Match 96.7%; Score 29; DB 2; Length 119;
 Best Local Similarity 83.3%; Pred. No. 90;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTGVR 6
 |||||
 Db 17 SGTGVR 22

RESULT 11

ID O9VVP3 PRELIMINARY; PRT: 119 AA.
 AC O9VVP3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CG15733 protein.
 GN CG15733.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;


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RN SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Cocayne J.D.,
RA Ananatiades P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKillop G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.A., Bouck J., Brockstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003488; AAF48149.1; -.
DR FlyBase: FBgn0030378; CG15733.
SQ SEQUENCE 119 AA; 12244 MW; 228A515283692840 CRC64;

Query Match 96.7%; Score 29; DB 5; Length 119;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
Db 6 SGTIGR 11
|||||

RESULT 12
Q8XU62 PRELIMINARY; PRT; 201 AA.
AC Q8XU62;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein RSC3331.
GN RSC3331 OR RS02565.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

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RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguiet P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL: AL646074; CAD17119.1; -.
DR InterPro: IPR002198; ADH_short.
DR PRINTS: PR00080; SDRFAMILY.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 201 AA; 20868 MW; 3EE0069C4BC9D069 CRC64;

Query Match 96.7%; Score 29; DB 16; Length 201;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
Db 9 SGTIGR 14
|||||

RESULT 13
Q8TUHO PRELIMINARY; PRT; 612 AA.
AC Q8TUHO;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glycyl-tRNA synthetase.
GN GLYS OR MA0097.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C2A; ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Pritchett M., Sowers K.R., Jing H., Macario A.J.L., Paulsen I.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL: AE010667; AAM03551.1; -.
KW Aminoacyl-tRNA synthetase; Complete proteome.
SQ SEQUENCE 612 AA; 69166 MW; A12AF972927C8B55 CRC64;

Query Match 96.7%; Score 29; DB 17; Length 612;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
Db 540 SGTIGR 545
|||||

RESULT 14
Q8RVQ5 PRELIMINARY; PRT; 829 AA.
AC Q8RVQ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

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DE SEC10.
 GN SEC10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ABOVE GROUND ORGANS;
 RA Elias M., Cvrckova F., Zarsky V.;
 RT "Molecular characterization of the exocyst complex in Arabidopsis
 thaliana";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF479280; AAL87123.1; --
 SQ SEQUENCE 829 AA; 90255 MW; 0CCCB0EE9CA5F536 CRC64;

Query Match 96.7%; Score 29; DB 10; Length 829;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SGTGVR 6
 |||:
 478 SGTIGR 483

RESULT 15
 Q94CK5 PRELIMINARY; PRT; 863 AA..
 AC Q94CK5;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical 93.9 kDa protein.
 GN AT5G12370.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
 RA Rudd S., Schoof H., Mayer K.F.X.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL592312; CAC42898.1;
 DR InterPro: IPR000873; AMP-bind.
 PROSITE: PS00455; AMP_BINDING; UNKNOWN_1.
 Hypothetical protein.
 SQ SEQUENCE 863 AA; 93929 MW; 2BBF48B1605FD577 CRC64;

Query Match 96.7%; Score 29; DB 10; Length 863;
 Best Local Similarity 83.3%; Pred. No. 6.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SGTGVR 6
 |||:
 Db 509 SGTIGR 514

Search completed: February 26, 2003, 08:39:41
 Job time : 23.9231 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:31:34 ; Search time 2.92308 Seconds
(without alignments)
85.136 Million cell updates/sec

Title: US-09-673-490B-1
Perfect score: 30
Sequence: 1 SGTVGR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query %	Match	Length	ID	Description
1	30	100.0	73	1	CXOD_CONCT	P58920 conus catus
2	30	100.0	406	1	DAC_STRSQ	P15555 streptomyc
3	30	100.0	758	1	SP21_YEAST	P35209 saccharomyc
4	30	100.0	911	1	DP01_MYCLE	P46835 mycobacteri
5	30	100.0	945	1	ERD1_ARATH	P42762 arabidopsis
6	29	96.7	377	1	MSK1_STRMU	Q00752 streptococc
7	29	96.7	385	1	T1S1_HAEIN	P71344 haemophilus
8	29	96.7	565	1	SYG_METTH	Q27874 methanobact
9	29	96.7	742	1	SYG_CAEEL	Q10039 caenorhabdi
10	29	96.7	745	1	ALD_HUMAN	P33897 homo sapien
11	27	90.0	246	1	PDX1_RHILO	Q98K16 rhizobium l
12	27	90.0	289	1	CR7B_THETH	P37270 thermus the
13	27	90.0	309	1	FN3X_HUMAN	Q9ha64 homo sapien
14	27	90.0	320	1	CELI_AGABI	Q00023 agarius bl
15	27	90.0	329	1	QOR_CAVPO	P11415 cavia porce
16	27	90.0	341	1	KHYB_ECOLI	P00557 escherichia
17	27	90.0	417	1	WNIA_HUMAN	Q9gzt5 homo sapien
18	27	90.0	417	1	WNIA_MOUSE	P70701 mus musculu
19	27	90.0	850	1	D7_DICDI	P54682 dictyosteli
20	26	86.7	116	1	WN52_EPTST	P28120 epatretus
21	26	86.7	123	1	WNT7_EVATR	P28092 evasterias
22	26	86.7	123	1	WNT7_STRPU	P28098 strongyloce
23	26	86.7	129	1	GALM_LACHE	Q00053 lactobacill
24	26	86.7	143	1	WNT1_EVATR	P28089 evasterias
25	26	86.7	221	1	RB27_RAT	P23640 rattus norv
26	26	86.7	223	1	NRFC_ECOLI	P32708 escherichia
27	26	86.7	253	1	YJ66_DEIRA	Q9rt03 deinococcus
28	26	86.7	261	1	YGD1_HAEIN	Q57097 haemophilus
29	26	86.7	274	1	TLIP_HUMAN	Q9h0e2 homo sapien
30	26	86.7	274	1	TLIP_MOUSE	Q9qz06 mus musculu
31	26	86.7	309	1	YDAA_HAEIN	P44195 haemophilus
32	26	86.7	315	1	YDAA_ECOLI	P03807 escherichia
33	26	86.7	414	1	HYUC_PESN	Q01264 pseudomonas

34	26	86.7	421	1	MTS1_STRFI	O52513 streptomyc
35	26	86.7	431	1	ENO_CLOAB	Q97152 clostridium
36	26	86.7	431	1	ENO_CLOPE	Q8xxu4 clostridium
37	26	86.7	445	1	SYG_BORBU	O51344 borrelia bu
38	26	86.7	457	1	YE07_MYCTU	P71675 mycobacteri
39	26	86.7	465	1	LIPP_HUMAN	P16233 homo sapien
40	26	86.7	465	1	LIPP_RABIT	Q02157 oryctolagus
41	26	86.7	485	1	Y136_TREPA	O83172 treponema p
42	26	86.7	500	1	LIPP_HUMAN	Q9v5x9 homo sapien
43	26	86.7	500	1	LIPP_MOUSE	Q9wvg5 mus musculu
44	26	86.7	502	1	EEA4_CAEEL	Q22682 caenorhabdi
45	26	86.7	517	1	PLIN_RAT	P43884 rattus norv

ALIGNMENTS

RESULT 1
CXOD_CONCT STANDARD; PRT; 73 AA.
AC P58920:
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Omega-conotoxin CVID precursor.
OS Conus catus (Cat cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_Taxid=101291;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 46-72, SYNTHESIS, AND STRUCTURE BY
NMR.
RC TISSUE=Venom duct, and Venom;
RX PubMed=10938268;
RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
RT "Novel omega-conotoxins from Conus catus discriminate among neuronal
calcium channel subtypes";
RL J. Biol. Chem. 275:35335-35344(2000).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
and block voltage-sensitive calcium channels (VSCC) (By
similarity). This toxin blocks N-type calcium channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
FAMILY.
KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
Amidation; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 45
FT PEPTIDE 46 72 OMEGA-CONOTOXIN CVID.
FT DISULFID 46 61 BY SIMILARITY.
FT DISULFID 53 65 BY SIMILARITY.
FT DISULFID 60 72 BY SIMILARITY.
FT MOD_RES 72 72 AMIDATION (G-73 PROVIDE AMIDE GROUP).
SQ SEQUENCE 73 AA; 7748 MW; C4CEBD30C77DAEC3 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
Db 66 SGTVGR 71

RESULT 2
DAC_STRSQ STANDARD; PRT; 406 AA.
ID DAC_STRSQ
AC P15555;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)
D-alanyl-D-alanine carboxypeptidase precursor (EC 3.4.16.4) (DD-peptidase) (DD-carboxypeptidase).
Streptomyces sp. (strain R61).
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces. NCBI_TaxID=1931;
[1]
SEQUENCE FROM N.A.
MEDLINE=87161818; PubMed=3830154;
Duez C., Piron-Praipont C., Joris B., Dusart J., Urdea M.S., Martial J.A., Frere J.-M., Ghuyssen J.-M.;
"Primary structure of the Streptomyces R61 extracellular DD-peptidase. 1. Cloning into Streptomyces lividans and nucleotide sequence of the gene.";
Eur. J. Biochem. 162:509-518(1987).
[2]
REVIEWS.
Duez C.;
Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
[3]
PARTIAL SEQUENCE.
MEDLINE=87161819; PubMed=3030739;
Joris B., Jacques P., Frere J.-M., Ghuyssen J.-M., van Beeumen J.;
"Primary structure of the Streptomyces R61 extracellular DD-peptidase. 2. Amino acid sequence data.";
Eur. J. Biochem. 162:519-524(1987).
[4]
X-RAY CRYSTALLOGRAPHY.
MEDLINE=90351121; PubMed=2386365;
Knox J.R., Pratt R.F.;
"Differential modes of vancomycin and D-alanyl-D-alanine peptidase binding to cell wall peptide and a possible role for the vancomycin resistance protein.";
Antimicrob. Agents Chemother. 34:1342-1437(1990).
[5]
X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=85207640; PubMed=3997832;
Kelly J.A., Knox J.R., Moews P.C., Hite G.J., Bartolone J.B., Zhao H., Joris B., Frere J.-M., Ghuyssen J.-M.;
"2.8-A Structure of penicillin-sensitive D-alanyl carboxypeptidase-transpeptidase from Streptomyces R61 and complexes with beta-lactams.";
J. Biol. Chem. 260:6449-6458(1985).
[6]
X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
MEDLINE=96083824; PubMed=7490745;
Kelly J.A., Kuzin A.P.;
"The refined crystallographic structure of a DD-peptidase penicillin-target enzyme at 1.6-A resolution.";
J. Mol. Biol. 254:223-236(1995).
-1- FUNCTION: CATALYZES DISTINCT CARBOXYPEPTIDATION AND PEPTIDOGLYCAN SYNTHESIS. MISTAKING A BETA-LACTAM ANTIBIOTIC MOLECULE FOR A NORMAL SUBSTRATE (I.E. A D-ALANYL-D-ALANINE-TERMINATED PEPTIDE), IT BECOMES IMMOBILIZED IN THE FORM OF A LONG-LIVED, SERINE-ESTER-LINKED ACYL ENZYME AND THUS BEHAVE AS PENICILLIN-BINDING PROTEIN (PBP).
-1- CATALYTIC ACTIVITY: D-alanyl-D-alanine + H(2)O = 2 D-alanine.
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S12; ALSO KNOWN AS THE D-ALANYL-D-ALANINE CARBOXYPEPTIDASE 2 FAMILY.

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EMBL; M26842; AAA62239.1; -

DR EMBL; X05109; CAA28756.1; -
DR PIR; S00765; S00765.
DR PDB; 2PTE; 31-JAN-94.
DR PDB; 3PTE; 15-AUG-95.
DR PDB; 1CEF; 14-OCT-96.
DR PDB; 1CEG; 14-OCT-96.
DR MEROPS; S12.001; -
KW Hydrolase; Carboxypeptidase; Peptidoglycan synthesis; Cell wall;
FT SIGNAL; 3D-structure.
FT CHAIN; 32 380 D-ALANYL-D-ALANINE CARBOXYPEPTIDASE.
FT PROPEP; 381 406
FT ACT_SITE; 93 93
SQ SEQUENCE 406 AA; 42917 MW; C2C77B53A29099E9 CRC64;
Query Match 100.0%; Score 30; DB 1; Length 406;
Best Local Similarity 100.0%; Pred. No. 27; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;
Oy 1 SGTVGR 6
| | | | |
Db 3 SGTVGR 8
RESULT 3
SP21_YEAST STANDARD; PRT; 758 AA.
AC P35209;
DT 01-FEB-1994 (Rel. 28, Created)
DI 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE SPT21 protein.
GN SPT21 OR YMR179W OR YMR8010.09.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=94186069; PubMed=8138180;
RX Natsoulis G., Winston F., Boeke J.D.;
"The SPT10 and SPT21 genes of Saccharomyces cerevisiae.";
RL Genetics 136:93-105(1994).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=S288C / AB972;
RA Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: REQUIRED FOR NORMAL TRANSCRIPTION AT A NUMBER OF LOCI IN YEAST.

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DR EMBL; L24436; AAA35078.1; -
DR EMBL; Z49808; CAA89912.1; -
DR PIR; S47866; S47866.
DR TRANSFAC; T04376; -
DR SGD; S0004791; SPT21.
FT DOMAIN; 127 144 ASP/GLU-RICH (ACIDIC).
FT DOMAIN; 672 682 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 758 AA; 84697 MW; 7DB3FCF7EE996705 CRC64;
Query Match 100.0%; Score 30; DB 1; Length 758;
Best Local Similarity 100.0%; Pred. No. 49; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;
Oy 1 SGTVGR 6

```

DR PFAM: PF02739; 5_3_exonuc_N; 1.
DR PRINTS: PR00868; DNAPOLI.
DR SMART: SM00474; 35EXOC; 1.
DR SMART: SM00475; 53EXOC; 1.
DR SMART: SM00279; HHH2; 1.
DR SMART: SM00482; POLAC; 1.
DR TIGRFS: TIGR00593; pola; 1.
DR PROSITE: PS00447; DNA_POLYMERASE_A; 1.
KW Transferase: DNA-directed DNA polymerase; DNA replication; DNA repair;
KW Hydrolase: Exonuclease; DNA-binding; Complete proteome.
SQ SEQUENCE 911 AA; 99791 MW; 12B4EAL8B2BC9864 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 911;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
DB 326 SGTVGR 331
|||||
|||||

RESULT 5
EXD1_ARATH
ID ERD1_ARATH STANDARD; PRT; 945 AA.
AC P42762;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ERD1 protein, chloroplast precursor.
GN ERD1 OR AT5G51070 OR K3K7.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RX MEDLINE=94071876; PubMed=7504470;
RA Kiyosue T., Yamaguchi-Shinozaki K., Shinozaki K.;
RT "Characterization of cDNA for a dehydration-inducible gene that
encodes a Clp A, B-like protein in Arabidopsis thaliana L.";
RL Biochem. Biophys. Res. Commun. 196:1214-1220(1993).
[2]
SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
features of the regions of 3,076,755 bp covered by sixty pl and TAC
clones.";
RL DNA Res. 7:31-63(2000).
CC -!- FUNCTION: MAY INTERACT WITH A CLPP-LIKE PROTEASE INVOLVED IN
CC DEGRADATION OF DENATURED PROTEINS IN THE CHLOROPLAST.
CC -!- SUBCELLULAR LOCATION: Chloroplast (Potential).
CC -!- INDUCTION: BY DEHYDRATION STRESS. INDUCED AFTER ONE HOUR OF
CC DEHYDRATION-STRESS AND REACHES MAXIMAL LEVELS AFTER 10 HOURS.
CC -!- SIMILARITY: BELONGS TO THE CLPA/CLPB FAMILY.
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-----
EMBL; D17582; BAA04506.1; -
EMBL; AB023044; BAB10330.1; -
EMBL; AB017063; BAB10330.1; JOINED.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.

DR PFAM: PF02739; 5_3_exonuc_N; 1.
DR PRINTS: PR00868; DNAPOLI.
DR SMART: SM00474; 35EXOC; 1.
DR SMART: SM00475; 53EXOC; 1.
DR SMART: SM00279; HHH2; 1.
DR SMART: SM00482; POLAC; 1.
DR TIGRFS: TIGR00593; pola; 1.
DR PROSITE: PS00447; DNA_POLYMERASE_A; 1.
KW Transferase: DNA-directed DNA polymerase; DNA replication; DNA repair;
KW Hydrolase: Exonuclease; DNA-binding; Complete proteome.
SQ SEQUENCE 911 AA; 99791 MW; 12B4EAL8B2BC9864 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 911;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
DB 326 SGTVGR 331
|||||
|||||

RESULT 4
DPOL_MYCLE
ID DPOL_MYCLE STANDARD; PRT; 911 AA.
AC P46835;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA polymerase I (EC 2.7.7.7) (POL I).
GN POLA OR MLI381.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=96059637; PubMed=7476188;
RA Fsihi H., Cole S.T.;
RT "The Mycobacterium leprae genome: systematic sequence analysis
identifies key catabolic enzymes, ATP-dependent transport systems and
a novel pola locus associated with genomic variability.";
RL Mol. Microbiol. 16:909-919(1995).
[2]
SEQUENCE FROM N.A.
RP SMITH D.R., Robison K.;
RA Submitter (SEP-1994) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RP STRAIN=TN;
RX MEDLINE=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies K.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -!- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE
CC EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY
CC (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + [DNA](N).
CC -!- SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS.
CC -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
-----
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-----
EMBL; D46257; CAA86364.1; -
EMBL; U00021; AAA50927.1; ALT_INIT.
DR EMBL; AL583921; CAC31762.1; -
DR HSP; P00582; 1KPD.
DR Leproma; MLI381; -
DR InterPro; IPR002562; 3_5_exonuclease.
DR InterPro; IPR002421; 5_3_exonuclease.
DR InterPro; IPR001098; DNA_pol.
DR InterPro; IPR002298; DNA_pol.
DR InterPro; IPR000513; EXO_N_1.
DR InterPro; IPR003584; HHH_2.
DR PFAM: PF00476; DNA_pol_A; 1.
DR PFAM: PF01367; 5_3_exonuclease; 1.

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DR InterPro: IPR001270; Chaprinin_clpA/B;
DR InterPro: IPR004176; Clp_N;
DR Pfam: PF000004; AAA; 2;
DR Pfam: PF02861; Clp_N; 2;
DR PRINTS: PR00300; CLPPROTEASEA;
DR PRODOM: PD000739; GSPIT_E; 1;
DR SMART: SM00382; AAA; 2;
DR PROSITE: PS00870; CLPAB_1; 1;
DR PROSITE: PS00871; CLPAB_2; 1;
DR PROSITE: PS00871; CLPAB_2; 1;
KW Chaperone; ATP-binding; Repeat; Chloroplast; Transit peptide.
FT TRANSIT 1 CHLOROPLAST (POTENTIAL).
FT CHAIN ? 945 ERD1 PROTEIN.
FT DOMAIN 271 523 I.
FT DOMAIN 590 781 II.
FT NP_BIND 316 323 ATP (POTENTIAL).
FT NP_BIND 664 671 ATP (POTENTIAL).
SQ SEQUENCE 945 AA; 103234 MW; 81EF2332C78F656B CRC64;

Query Match 100.0%; Score 30; DB 1; Length 945;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTGVR 6
   |||||
   395 SGTGVR 400

RESULT 6
MSMK_STRMU STANDARD; PRT; 377 AA.
ID MSMK_STRMU
AC Q00752;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Multiple sugar-binding transport ATP-binding protein msmk.
GN MSMK.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ingbritt;
RX MEDLINE=92165821; PubMed=1537846;
RA Russell R.R.B., Aduse-Opoku J., Sutcliffe I.C., Tao L.,
RA Ferretti J.J.;
RT "A binding protein-dependent transport system in Streptococcus mutans
RT responsible for multiple sugar metabolism.";
RL J. Biol. Chem. 267:4631-4637(1992).
CC -!- FUNCTION: INVOLVED IN A BINDING PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC RESPONSIBLE FOR THE UPTAKE OF MELIBIOSE, RAFFINOSE AND
CC ISOMALTOTRIOSE. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE
CC TRANSPORT SYSTEM.
CC -!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
CC
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CC
CC EMBL; M77351; AAA26938.1; -.
CC PIR; E42400; E42400.
CC InterPro: IPR003593; AAA_ATPase.
CC InterPro: IPR003439; ABC_Transportr.
CC InterPro: IPR005116; TOBE.
CC Pfam; PF000005; ABC_tran; 1.
CC Pfam; PF03459; TOBE; 1.
CC PRODOM: PD000006; ABC_transportr; 1.
CC SMART; SM00382; AAA; 1.

DR PROSITE; PS00211; ABC_TRANSPORTER; 1;
DR Transport; Sugar transport; Membrane; ATP-binding.
KW NP_BIND 38 45 ATP (BY SIMILARITY).
SQ SEQUENCE 377 AA; 41964 MW; 640FAD09228736A CRC64;

Query Match 96.7%; Score 29; DB 1; Length 377;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTGVR 6
   |||||
   218 SGTGVR 223

RESULT 7
TISI_HAEIN STANDARD; PRT; 385 AA.
ID TISI_HAEIN
AC P71344;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative type I restriction enzyme specificity protein HI0216 (S
DE protein).
DE HI0216.
GN Haemophilus influenzae.
OS Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus
OC Haemophilus
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Spriggs T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: THE M AND S SUBUNITS TOGETHER FORM A METHYLTRANSFERASE
CC (MTASE) THAT METHYLATES TWO ADENINE RESIDUES IN COMPLEMENTARY
CC STRANDS OF BIPARTITE DNA RECOGNITION SEQUENCE. SUBUNIT S DICTATES
CC DNA SEQUENCES SPECIFICITY (BY SIMILARITY).
CC -!- SUBUNIT: THE TYPE I RESTRICTION & MODIFICATION SYSTEM IS COMPOSED
CC OF THREE POLYPEPTIDES R, M AND S (BY SIMILARITY).
CC -!- DOMAIN: CONTAINS TWO DNA RECOGNITION DOMAINS, EACH SPECIFYING
CC RECOGNITION OF ONE OF THE TWO DEFINED COMPONENTS OF THE TARGET
CC SEQUENCE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TYPE-I RESTRICTION SYSTEM S METHYLASE
CC FAMILY.
CC
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CC
CC EMBL; U32706; AAC21883.1; -.
CC REBASE; 3654; S.Hindorf215P.
CC TIGR; HI0216; -.
CC InterPro: IPR000055; Methylase_S.
CC Pfam; PF01420; Methylase_S; 2.
KW Hypothetical protein; Restriction system; DNA-binding; Repeat;
KW Complete proteome.
SQ SEQUENCE 385 AA; 44277 MW; AD6A5D037961E62F CRC64;

```

Query Match 96.7%; Score 29; DB 1; Length 385;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTGVR 6
|||:|
Db 268 SGTIGR 273

RESULT 8

```
SYG_METH      STANDARD;      PRT;      565 AA.
AC 027874;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE GLYCYL-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).
GN GLYS OR MTH1846.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics."
RL J. Bacteriol. 179:7135-7153(1997).
CC -!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
CC + glycyI-tRNA(Gly).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; AE000937; AAB86312.1; -
CC HSSP; P56206; 1AT1.
CC InterPro; IPR002106; AATRNA_ligaseII.
CC InterPro; IPR004154; HGTP_anticonodon.
CC InterPro; IPR002314; tRNA-synt_2b.
CC InterPro; IPR002315; tRNA-synt_gly.
CC Pfam; PF00587; tRNA-synt_2b; 1.
CC Pfam; PF03129; HGTP_anticonodon; 1.
CC PRINTS; PR01043; TRNASYNTHGLY.
CC TIGRFAMs; TIGR00389; glyS_dimeric; 1.
CC PROSITE; PS00862; AA-TRNA_LIGASE-II; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 565 AA; 64799 MW; D95C082C893A2CBA CRC64;
```

Query Match 96.7%; Score 29; DB 1; Length 565;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTGVR 6
|||:|
Db 507 SGTIGR 512

RESULT 9

```
SYG_CAEL      STANDARD;      PRT;      742 AA.
AC Q10039;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE GLYCYL-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).
GN GRS-1 OR t10F2.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Miller N.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
CC + glycyI-tRNA(Gly).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -!- SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.
CC -----
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CC -----
CC EMBL; U23412; AAK21465.2; -
CC HSSP; P56206; 1AT1.
CC WormPep; t10F2.1; CE29472.
CC InterPro; IPR002106; AATRNA_ligaseII.
CC InterPro; IPR004154; HGTP_anticonodon.
CC InterPro; IPR000738; WHEP-TRS.
CC InterPro; IPR002314; tRNA-synt_2b.
CC InterPro; IPR002315; tRNA-synt_gly.
CC Pfam; PF00458; WHEP-TRS; 1.
CC Pfam; PF00587; tRNA-synt_2b; 1.
CC Pfam; PF03129; HGTP_anticonodon; 1.
CC PRINTS; PR01043; TRNASYNTHGLY.
CC TIGRFAMs; TIGR00389; glyS_dimeric; 1.
CC PROSITE; PS00762; AA-TRNA_LIGASE-II; 1.
CC PROSITE; PS00762; WHEP-TRS; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT DOMAIN 84 129 WHEP-TRS.
SQ SEQUENCE 742 AA; 84149 MW; 8FAC5C407AB4F2B7 CRC64;
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Query Match 96.7%; Score 29; DB 1; Length 742;
Best Local Similarity 83.3%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTGVR 6
|||:|
Db 661 SGTIGR 666

RESULT 10

```
ALD_HUMAN
ID ALD_HUMAN      STANDARD;      PRT;      745 AA.
AC P33897;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adrenoleukodystrophy protein (ALDP).
GN ABCD1 OR ALD.
```

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93180910; PubMed=8441467;
 RA Mosser J., Douar A.-M., Sarde C.-O., Kioschis P., Feil R., Moser H.,
 RA Poustka A.-M., Mandel J.-L., Aubourg P.;
 RT "Putative X-linked adrenoleukodystrophy gene shares unexpected
 RT homology with ABC transporters.";
 RL Nature 361:726-730(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Platzter M., Bauer D., Brenner V., Drescher B., Nyakatura G.,
 RA Reichwald K., Sandoval N., Coy J., Kioschis P., Korn B.,
 RA Poustka A.-M., Rosenthal A.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SUBUNITS, AND CHARACTERIZATION OF VARIANTS X-ALD H-389; Q-401; R-484
 RP AND Q-591.
 RX MEDLINE=20020240; PubMed=10551832;
 RA Liu L.X., Janvier K., Berteaux-Lecellier V., Cartier N., Benarous R.,
 RA Aubourg P.;
 RT "Homo- and heterodimerization of peroxisomal ATP-binding cassette
 RT half-transporters.";
 RL J. Biol. Chem. 274:32738-32743(1999).
 RN [4]
 RP FUNCTION, AND CHARACTERIZATION OF VARIANTS X-ALD SER-512 AND LEU-606.
 RX MEDLINE=21145507; PubMed=11248239;
 RA Roedig P., Mayerhofer P., Hozinger A., Gaertner J.;
 RT "Characterization and functional analysis of the nucleotide binding
 RT fold in human peroxisomal ATP binding cassette transporters.";
 RL FEBS Lett. 492:66-72(2001).
 RN [5]
 RP REVIEW
 RX MEDLINE=93283453; PubMed=8507690;
 RA Aubourg P., Mosser J., Douar A.-M., Sarde C.-O., Lopez J.,
 RA Mandel J.-L.;
 RT "Adrenoleukodystrophy gene: unexpected homology to a protein involved
 RT in peroxisome biogenesis.";
 RL Biochimie 75:293-302(1993).
 RN [6]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=97338663; PubMed=9195223;
 RA Dodd A., Rowland S.A., Hawkes S.L.J., Kennedy M.A., Love D.R.;
 RT "Mutations in the adrenoleukodystrophy gene.";
 RL Hum. Mutat. 9:500-511(1997).
 RN [7]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=21614879; PubMed=11748843;
 RA Kemp S., Pujoil A., Waterham H.R., van Geel B.M., Boehm C.D.,
 RA Raymond G.V., Cutting G.R., Wanders R.J.A., Moser H.W.;
 RT "ABCDI mutations and the X-linked adrenoleukodystrophy mutation
 RT database: role in diagnosis and clinical correlations.";
 RL Hum. Mutat. 18:499-515(2001).
 RN [8]
 RP VARIANT X-ALD LYS-291.
 RX MEDLINE=94108454; PubMed=7904210;
 RA Cartier N., Sarde C.-O., Douar A.-M., Mosser J., Mandel J.-L.,
 RA Aubourg P.;
 RT "Abnormal messenger RNA expression and a missense mutation in
 RT patients with X-linked adrenoleukodystrophy.";
 RL Hum. Mol. Genet. 2:1949-1951(1993).
 RN [9]
 RP VARIANTS X-ALD SER-148; ASP-174; ARG-266; GLN-401; TRP-418 AND
 RP PHE-515.
 RX MEDLINE=95152524; PubMed=7849723;
 RA Fuchs S., Sarde C.-O., Wedemann H., Schwinger E., Mandel J.-L.,
 RA Gal A.;
 RT "Missense mutations are frequent in the gene for X-chromosomal
 RT adrenoleukodystrophy (ALD).";
 RL Hum. Mol. Genet. 3:1903-1905(1994).
 RN [10]
 RP VARIANTS X-ALD TRP-518; LEU-606; CYS-617 AND HIS-617.
 RX MEDLINE=94314951; PubMed=8040304;
 RA Fanen P., Guidoux S., Sarde C.-O., Mandel J.-L., Goossens M.,
 RA Aubourg P.;
 RT "Identification of mutations in the putative ATP-binding domain of
 RT the adrenoleukodystrophy gene.";
 RL J. Clin. Invest. 94:516-520(1994).
 RN [11]
 RP VARIANTS X-ALD.
 RX MEDLINE=95126139; PubMed=7825602;
 RA Ligtgenberg M.J.L., Kemp S., Sarde C.-O., van Geel B.M., Kleijer W.J.,
 RA Barth P.G., Mandel J.-L., van Oost B.A., Bolhuis P.A.;
 RT "Spectrum of mutations in the gene encoding the adrenoleukodystrophy
 RT protein.";
 RL Am. J. Hum. Genet. 56:44-50(1995).
 RN [12]
 RP VARIANTS X-ALD HIS-104; GLU-178; LEU-560 AND GLY-528 DEL.
 RX MEDLINE=95233433; PubMed=7717396;
 RA Braun A., Ambach H., Kammerer S., Rollinski B., Stoeckler S., Rabl W.,
 RA Gaertner J., Zierz S., Roscher A.A.;
 RT "Mutations in the gene for X-linked adrenoleukodystrophy in patients
 RT with different clinical phenotypes.";
 RL Am. J. Hum. Genet. 56:854-861(1995).
 RN [13]
 RP VARIANTS X-ALD.
 RX MEDLINE=96047143; PubMed=7581394;
 RA Kok F., Neumann S., Sarde C.-O., Zheng S., Wu K.-H., Wei H.-M.,
 RA Bergin J., Watkins P.A., Gould S., Sack G., Moser H., Mandel J.-L.,
 RA Smith K.D.;
 RT "Mutational analysis of patients with X-linked adrenoleukodystrophy.";
 RL Hum. Mutat. 6:104-115(1995).
 RN [14]
 RP VARIANTS X-ALD.
 RX MEDLINE=96213748; PubMed=8651290;
 RA Feigenbaum V., Lombard-Platet G., Guidoux S., Sarde C.-O.,
 RA Mandel J.-L., Aubourg P.;
 RT "Mutational and protein analysis of patients and heterozygous women
 RT with X-linked adrenoleukodystrophy.";
 RL Am. J. Hum. Genet. 58:1135-1144(1996).
 RN [15]
 RP VARIANTS X-ALD.
 RX MEDLINE=96163493; PubMed=8566952;
 RA Krasemann E.W., Meier V., Korenke G.C., Hunneman D.H., Hanefeld F.;
 RT "Identification of mutations in the ALD-gene of 20 families with
 RT adrenoleukodystrophy/adrenomyeloneuropathy.";
 RL Hum. Genet. 97:194-197(1996).
 RN [16]
 RP VARIANT AMN ARG-679.
 RX MEDLINE=98112466; PubMed=9452087;
 RA Korenke G.C., Krasemann E., Meier V., Beuche W., Hunneman D.H.,
 RA Hanefeld F.;
 RT "First missense mutation (W679R) in exon 10 of the
 RT adrenoleukodystrophy gene in siblings with adrenomyeloneuropathy.";
 RL Hum. Mutat. Suppl. 1:S204-S206(1998).
 RN [17]
 RP VARIANTS X-ALD.
 RX MEDLINE=99408241; PubMed=10480364;
 RA Wichers M., Kohler W., Brenemann W., Boese V., Sokolowski P.,
 RA Biallingmaier F., Ludwig M.;
 RT "X-linked adrenomyeloneuropathy associated with 14 novel ALD-gene
 RT mutations: no correlation between type of mutation and age of onset.";
 RL Hum. Genet. 105:116-119(1999).
 RN [18]
 RP VARIANTS X-ALD LEU-108 AND SER-143.
 RX MEDLINE=99299442; PubMed=10369742;
 RA Perusi C., Gomez-Lira M., Mottes M., Pignatti P.F., Bertini E.,
 RA Cappa M., Vigliani M.C., Schiffer D., Rizzuto N., Salvati A.;
 RT "Two novel missense mutations causing adrenoleukodystrophy in Italian
 RT patients.";
 RL Mol. Cell. Probes 13:179-182(1999).
 RN [19]
 RP VARIANTS X-ALD.


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RX MEDLINE=20202141; PubMed=10737980;
RA Lachtermacher M.B., Seunanez H.N., Moser A.B., Moser H.W., Smith K.D.;
RT "determination of 30 x-linked adrenoleukodystrophy mutations,
RT including 15 not previously described.";
RL Hum. Mutat. 15:348-353(2000).
[20]
RN VARIANTS X-ALD GLN-401; TRP-418; LEU-543 AND ARG-556.
RX MEDLINE=20438355; PubMed=10980539;
RA Lira M.G., Mottes N., Pignatti P.F., Medica I., Uziel G., Cappa M.,
RA Bertini E., Rizzuto N., Salvati A.;
RT "Detection of mutations in the ALD gene (ABCD1) in seven Italian
RT families: description of four novel mutations.";
RL Hum. Mutat. 16:271-271(2000).
[21]
RN VARIANTS X-ALD L-98; D-99; E-217; Q-518; D-608; I-633 AND P-660, AND
RX MEDLINE=T-13.
RA MEDLINE=21331689; PubMed=11438993;
RA Dvorakova L., Storkanova G., Unterrainer G., Hujova J., Kmoch S.,
RA Zeman J., Hrebicek M., Berger J.;
RT "Eight novel ABCD1 gene mutations and three polymorphisms in patients
RT with x-linked adrenoleukodystrophy: The first polymorphism causing an
RT amino acid exchange.";
RL Hum. Mutat. 18:52-60(2001).
[22]
RN VARIANTS X-ALD 300-VAL-GLY-GLN INS.
RX MEDLINE=21668186; PubMed=11810273;
RA Guimaraes C.P., Lemos M., Menezes I., Coelho T., Sa-Miranda C.,
RA Azevedo J.E.;
RT "Characterisation of two mutations in the ABCD1 gene leading to low
RT levels of normal ALDP.";
RL Hum. Genet. 109:616-622(2001).
CC AS AN ATP-BINDING SUBUNIT WITH ATPASE ACTIVITY.
CC AS AN ATP-BINDING SUBUNIT WITH ATPASE ACTIVITY.
CC -!- FUNCTION: PROBABLE TRANSPORTER. THE NUCLEOTIDE-BINDING FOLD ACTS
CC -!- SUBUNIT: CAN FORM HOMO- AND HETERODIMERS WITH ABCD2/ALDR AND
CC ABCD3/PMP70. DIMERIZATION IS NECESSARY TO FORM AN ACTIVE
CC TRANSPORTER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal.
CC -!- DISEASE: DEFECTS IN ABCD1 ARE THE CAUSE OF RECESSIVE X-LINKED
CC ADRENOLEUKODYSTROPHY (X-ALD), A RARE PEROXISOMAL METABOLIC
CC DISORDER THAT OCCURS IN BOYS AND IS CHARACTERIZED BY PROGRESSIVE
CC MULTIFOCAL DEMYELINATION OF THE CENTRAL NERVOUS SYSTEM AND BY
CC ADRENOCORTICAL INSUFFICIENCY. IT PRODUCES MENTAL DETERIORATION,
CC CORTICOSPINAL TRACT DYSFUNCTION, AND CORTICAL BLINDNESS. THERE IS
CC LABORATORY EVIDENCE OF ADRENAL CORTICAL DYSFUNCTION. DIFFERENT
CC CLINICAL MANIFESTATIONS EXIST LIKE: CEREBRAL CHILDHOOD ALD (CALD),
CC ADULT CEREBRAL ALD (ACALD), ADRENOMYELONEUROPATHY (AMN) AND
CC "ADDISON DISEASE ONLY" (ADO) PHENOTYPE.
Query Match 96.7%; Score 29; DB 1; Length 745;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGTGVR 6
DB 447 SGTIGR 452
RESULT 11
PDXJ_RHILO
ID PDXJ_RHILO STANDARD; PRT; 246 AA.
AC Q98KL6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Pyridoxal phosphate biosynthetic protein pdxJ (PMP synthase).
GN PDXJ OR MLL1418.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;

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RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
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CC
CC EMBL; AP002997; BAB48798.1;
KW Pyridoxine biosynthesis; Complete proteome.
SQ SEQUENCE 246 AA; 26419 MW; 69DE563CBDAE3FA80 CRC64;
Query Match 90.0%; Score 27; DB 1; Length 246;
Best Local Similarity 83.3%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGTGVR 6
DB 234 AGIVGR 239
RESULT 12
CRTB_THETH
ID CTRB_THETH STANDARD; PRT; 289 AA.
AC P37270;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytoene synthase (EC 2.5.1.-).
GN CTRB.
OS Thermus thermophilus.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
OC Thermaceae; Thermus.
OX NCBI_TaxID=274;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=HB27;
RX MEDLINE=94028944; PubMed=8215386;
RA Hoshino T., Fujii R., Nakahara T.;
RT "Molecular cloning and sequence analysis of the crtB gene of Thermus
RT thermophilus HB27, an extreme thermophile producing carotenoid
RT pigments.";
RL Appl. Environ. Microbiol. 59:3150-3153(1993).
CC -!- FUNCTION: CATALYZES THE REACTION FROM PREPHYTOENE DIPHOSPHATE
CC TO PHYTOENE.
CC -!- CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate +
CC prephytoene diphosphate.
CC -!- CATALYTIC ACTIVITY: Prephytoene diphosphate = diphosphate +
CC phytoene.
CC -!- PATHWAY: Carotenoid biosynthesis.
CC -!- SIMILARITY: BELONGS TO THE PHYTOENE/SQUALENE SYNTHETASE FAMILY.
CC
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CC
CC EMBL; AB001637; -; NOT_ANNOTATED_CDS.
DR InterPro: IPR002060; Squ/phyt_synthse.
DR Pfam: PF00494; SQS_PSY; 1.

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DR PROSITE; PS01044; SQUALEN_PHYTOEN_SYN_1; 1.
DR PROSITE; PS01045; SQUALEN_PHYTOEN_SYN_2; 1.
KW Multifunctional enzyme; Carotenoid biosynthesis; Transferase.
SQ SEQUENCE 289 AA; 31964 MW; 3F58C1141902D3C5 CRC64;

Query Match
Best Local Similarity 90.0%; Score 27; DB 1; Length 289;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
DB 131 AGTVGR 136

RESULT 13
FN3X_HUMAN STANDARD; PRT; 309 AA.
ID Q9HAG6; Q9H07;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hypothetical fructosamine kinase-like protein FLJ12171/DKFP564D202.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Nomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 1-197 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21154917; PubMed=11230166;
RA Wilmann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansgore W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Meves H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
[3]
RP SEQUENCE OF 136-309 FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE FRUCTOSAMINE KINASE FAMILY.
-----
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-----
DR EMBL; AK022233; BAB13992.1; -
DR EMBL; AL136631; CAB66566.1; -
DR EMBL; BC001458; AA01458.1; -
KW Hypothetical protein; Transferase; Kinase.
FT CONFLICT 129 129 G -> W (IN REF. 2).
FT CONFLICT 136 138 ERP -> HEA (IN REF. 3).
FT CONFLICT 265 265 G -> C (IN REF. 3).
FT CONFLICT 278 278 R -> Q (IN REF. 3).

SQ SEQUENCE 309 AA; 34440 MW; C34ED1C5BB2A7FF0 CRC64;

Query Match
Best Local Similarity 90.0%; Score 27; DB 1; Length 309;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
DB 125 AGTVGR 130

RESULT 14
CELL_AGABI STANDARD; PRT; 320 AA.
ID CELL_AGABI
AC Q00023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellulose-growth-specific protein precursor.
GN CELL.
OS Agaricus bisporus (Common mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Agaricaceae; Agaricus.
OX NCBI_TaxID=5341;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D649;
RX MEDLINE=93012985; PubMed=1398098;
RA Raguz S., Yaguee E., Wood D.A., Thurston C.F.;
RT "Isolation and characterization of a cellulose-growth-specific gene
RL from Agaricus bisporus.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D649;
RX MEDLINE=94237428; PubMed=8181702;
RA Arnesilla A.L., Thurston C.F., Yaguee E.;
RT "CELL: a novel cellulose binding protein secreted by Agaricus
RT bisporus during growth on crystalline cellulose.";
RL FEMS Microbiol. Lett. 116:293-299(1994).
CC -!- FUNCTION: PROBABLE GLYCOSYL HYDROLASE ACTIVE ON CELLULOSE.
CC -!- SUBCELLULAR LOCATION: Secreted
CC -!- SIMILARITY: BELONGS TO FAMILY 61 OF GLYCOSYL HYDROLASES.
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-----
DR EMBL; M86356; AAA53434.1; -
DR HSSP; P00725; 2CBH.
DR InterPro; IPR000254; CBD_fungal.
DR InterPro; IPR005103; Glyco_hydro_61.
DR Pfam; PF00734; CBM.1; 1.
DR Pfam; PF03443; Glyco_hydro_61; 1.
DR SMART; SM00236; ICB; 1.
DR PROSITE; PS00562; CBD_FUNGAL; 1.
KW Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 320 CELLULOSE-GROWTH-SPECIFIC PROTEIN.
FT DOMAIN 30 261 CATALYTIC (POTENTIAL).
FT DOMAIN 262 285 LINKER (POTENTIAL).
FT DOMAIN 286 320 CELLULOSE-BINDING (POTENTIAL).
FT DISULFID 292 309 BY SIMILARITY.
FT DISULFID 303 319 BY SIMILARITY.
FT CARBOHYD 163 163 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 320 AA; 33754 MW; 60E2C8080895CA2B CRC64;

Query Match
Score 27; DB 1; Length 320;
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Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
DB 146 SGTVGK 151

RESULT 15
QOR_CAVPO STANDARD; PRT; 329 AA.
AC P11415;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (zeta-
DE crystallin).
GN CRYZ.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=89378748; PubMed=2777081;
RA Rodokanaki A., Holmes R.K., Borrás T.;
RT "Zeta-crystallin, a novel protein from the guinea pig lens is related
RT to alcohol dehydrogenases.";
RL Gene 78:215-224(1989).
RN [2]
RP CHARACTERIZATION.
RC TISSUE=Liver;
RX MEDLINE=93041895; PubMed=1420281;
RA Rao P.V., Zigler J.S. Jr.;
RT "Purification and characterization of zeta-crystallin/quinone
RT reductase from guinea pig liver.";
RL Biochim. Biophys. Acta 1117:315-320(1992).
RN [3]
RP CHARACTERIZATION.
RC TISSUE=Liver;
RX MEDLINE=92112732; PubMed=1370456;
RA Rao P.V., Krishna C.M., Zigler J.S. Jr.;
RT "Identification and characterization of the enzymatic activity of
RT zeta-crystallin from guinea pig lens. A novel NADPH:quinone
RT oxidoreductase.";
RL J. Biol. Chem. 267:96-102(1992).
CC -!- FUNCTION: DOES NOT HAVE ALCOHOL DEHYDROGENASE ACTIVITY. BINDS
CC NADP AND ACTS THROUGH A ONE-ELECTRON TRANSFER PROCESS.
CC ORTHOQUINONES ARE THE BEST SUBSTRATES. MAY ACT IN THE
CC DETOXIFICATION OF XENOBIOTICS.
CC -!- CATALYTIC ACTIVITY: NADPH + quinone = NADP(+) + semiquinone.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: IN GUINEA PIGS IT CONSTITUTES ABOUT 10% OF THE
CC WATER SOLUBLE PROTEINS OF THE LENS.
CC -!- DISEASE: A GENOMIC MUTATION CAUSING THE DELETION OF 34 AMINO ACIDS
CC WAS CLEARLY ASSOCIATED WITH A HEREDITARY NUCLEAR CATARACT IN A
CC LINE OF STRAIN 13 GUINEA PIGS.
CC -!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY. QUINONE OXIDOREDUCTASE SUBFAMILY.
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-----
CC EMBL: M26936; AAA37035.1; -
CC PIR: JS0230; CYGPZ.
CC HSSP: P28304; IQOR.
CC InterPro: IPR002085; Adh_zn_family.

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DR InterPro: IPR002364; QOR_zeta_crystal.
DR Pfam: PF00107; adh_zinc; 1.
DR PROSITE: PS01162; QOR_ZETA_CRYSTAL; 1.
KW Oxidoreductase; NADP; zinc; Eye lens protein.
SQ SEQUENCE 329 AA; 35202 MW; 1463632C672C234F CRC64;

Query Match 90.0%; Score 27; DB 1; Length 329;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
DB 319 SGTVGK 324

Search completed: February 26, 2003, 08:37:17
Job time : 4.92308 secs

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OM protein - protein search, using sw model

Run on: February 26, 2003, 08:32:54 ; Search time 5.53846 Seconds
(without alignments)
104.146 Million cell updates/sec

Title: US-09-673-490B-1
Perfect score: 30
Sequence: 1. SGTVGR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	204	2 A48725	nuclear DNA-bindin
2	30	100.0	206	2 B69002	hypothetical prote
3	30	100.0	324	2 T51219	hypothetical prote
4	30	100.0	358	2 C82281	ferric vibriobacti
5	30	100.0	406	1 S48220	serine-type D-Ala-
6	30	100.0	711	2 C70606	probable fadE34 pr
7	30	100.0	758	2 S47866	SPT21 protein - ve
8	30	100.0	911	2 S77659	DNA-directed DNA p
9	30	100.0	945	2 JN0901	endopeptidase Clp
10	29	96.7	377	2 E42400	ABC-type transport
11	29	96.7	385	2 E64055	hypothetical prote
12	29	96.7	565	2 H69113	glycine-tRNA ligas
13	29	96.7	745	2 G02500	probable transport
14	29	96.7	746	2 T16843	hypothetical prote
15	27	90.0	109	2 I52333	GI phase-specific
16	27	90.0	138	2 G71065	hypothetical prote
17	27	90.0	140	2 B72480	hypothetical prote
18	27	90.0	141	2 D82745	hypothetical prote
19	27	90.0	256	2 B69197	conserved hypothet
20	27	90.0	320	2 JCI311	cell protein precu
21	27	90.0	327	2 G88976	protein F34E2.6 [i
22	27	90.0	328	2 A83219	probable transmemb
23	27	90.0	329	1 CYGPF	zeta-crystallin /
24	27	90.0	341	1 WGECH	hygromycin-B kinas
25	27	90.0	378	2 E86677	hypothetical prote
26	27	90.0	388	2 F89773	hypothetical prote
27	27	90.0	417	2 B59392	Wnt10a protein pro
28	27	90.0	417	2 JC7693	soluble-type glyco
29	27	90.0	441	2 S76513	hypothetical prote

30 27 90.0 506 2 F83545
31 27 90.0 524 2 D82944
32 27 90.0 540 2 T08662
33 27 90.0 541 2 T34850
34 27 90.0 559 2 D95055
35 27 90.0 559 2 A97925
36 27 90.0 632 2 T22052
37 27 90.0 670 2 JC5887
38 27 90.0 756 2 JC5886
39 27 90.0 1014 2 JE0333
40 27 90.0 1073 1 T08228
41 27 90.0 1140 2 B97820
42 27 90.0 1152 2 E71667
43 27 90.0 1400 2 T22644
44 27 90.0 1868 2 T23707
45 26 86.7 113 2 C70691

ALIGNMENTS

RESULT 1

A48725
nuclear DNA-binding protein - Marek's disease virus
C:Species: Marek's disease virus
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A48725
R:Camp, H.S.; Silva, R.F.; Coussens, P.M.
Virology 196, 484-495, 1993
A:Title: Defective Marek's disease virus DNA contains a gene encoding a potential
A:Reference number: A48725; MUID:93383373; PMID:8396799
A:Accession: A48725
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-204 <CAM>
A:Cross-references: GB:L10087; NID:g306312; PIDN:AAA46121.1; PID:g306313
A:Experimental source: serotype 2, 281M1/1
A>Note: sequence extracted from NCBI backbone (NCBIN:137884, NCBIP:137885)

Query Match 100.0%; Score 30; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
DB 139 SGTVGR 144

RESULT 2

B69002
hypothetical protein MTH1013 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: B69002
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, J.
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: f
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: B69002
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-206 <MTH>
A:Cross-references: GB:AE000874; GB:AE000666; NID:g2622110; PIDN:AAB85509.1; PID:g2622110
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1013

Query Match 100.0%; Score 30; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6
|||||

Db 21 SGTVGR 26

RESULT 3

T51219

hypothetical protein B24M22.150 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 08-Sep-2000

C:Accession: T51219

R:Schultze, U.; Aign, V.; Hoheisel, J.; Brändt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, July 2000

A:Reference number: Z25286

A:Accession: T51219

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-324 <SCH>

A:Cross-references: EMBL:AL390354; GSPDB:GN00116; NCSP:B24M22.150

A:Experimental source: strain OR74A

C:Genetics:

A:Gene: NCSP:B24M22.150

A:Map position: 6

A:Introns: 121/2; 135/1; 202/2

Superfamily: Neurospora crassa hypothetical protein B24M22.150

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 324;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6

|||||

Db 54 SGTVGR 59

RESULT 4

C82281

ferric vibriobactin ABC transporter, permease protein VC0778 [imported] - Vibrio cholerae

C:Species: Vibrio cholerae

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: C82281

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, R.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: C82281

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <HEI>

A:Cross-references: GB:AE004163; GB:AE003852; NID:g9655221; PIDN:AAF93943.1; GSPDB:GN001

Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0778

A:Map position: 1

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 358;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6

|||||

Db 167 SGTVGR 172

RESULT 5

S48220

serine-type D-Ala-D-Ala carboxypeptidase (EC 3.4.16.4) precursor - Streptomyces sp.

N:Alternate names: D-alanyl-D-alanine carboxypeptidase; DD-peptidase

C:Species: Streptomyces sp.

C>Date: 15-Jul-1995 #sequence_revision 11-Apr-1997 #text_change 18-Jun-1999

C:Accession: S48220; S00765; S11947

R:Duez, C.; Piron-Fraipont, C.; Joris, B.; Dusart, J.; Urdea, M.S.; Martial, J.A.; Fr
Eur. J. Biochem. 224, 1079, 1994

A:Title: Correction. Primary structure of the Streptomyces R61 extracellular DD-pepti

A:Reference number: S48220; MUID:95010068; PMID:7925404

A:Accession: S48220

A:Molecule type: DNA

A:Residues: 1-406 <DUEL>

A:Cross-references: GB:M26842; NID:g153447; PIDN:AAA62239.1; PID:g153448.

A>Note: Correction to sequence S00765

R:Duez, C.; Piron-Fraipont, C.; Joris, B.; Dusart, J.; Urdea, M.S.; Martial, J.A.; Fr

Eur. J. Biochem. 162, 509-518, 1987

A:Title: Primary structure of the Streptomyces R61 extracellular DD-peptidase. 1. Clo

A:Reference number: S00765; MUID:87161818; PMID:3830154

A:Accession: S00765

A:Molecule type: DNA

A:Residues: 1-266, 'TGA', 270-346, 'QAH', 350-380, 'GEAAQRDLGDRGAP', 397-406 <DUE2>

A:Cross-references: EMBL:X05109; GB:M26842; NID:g515049

R:Piron-Fraipont, C.; Lenzi, M.V.; Dusart, J.; Ghuyssen, J.M.

Mol. Gen. Genet. 223, 114-120, 1990

A:Title: Transcriptional analysis of the DD-peptidase/penicillin-binding protein-enco

A:Reference number: S11947; MUID:91080851; PMID:2175384

A:Accession: S11947

A:Molecule type: DNA

A:Residues: 1-91; 171-173 <PTR>

A:Cross-references: EMBL:X55810; NID:g296314

C:Function:

A:Description: catalyzes the hydrolysis of carboxyl-terminal D-alanyl-D-alanyl peptid

C:Superfamily: Escherichia coli beta-lactamase

C:Keywords: hydrolase; serine carboxypeptidase

F:1-31/Domain: signal sequence #status predicted <SIG>

F:32-380/Product: serine-type D-Ala-D-Ala carboxypeptidase #status predicted <MAT>

F:381-406/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:93/Active site: Ser #status predicted

Query Match 100.0%; Score 30; DB 1; Length 406;

Best Local Similarity 100.0%; Pred. No. 56;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6

|||||

Db 3 SGTVGR 8

RESULT 6

C70606

probable fadE34 protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: C70606

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: C70606

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-711 <COL>

A:Cross-references: GB:922774; GB:AL123456; NID:g3261729; PIDN:CAB07147.1; PID:e30671

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: fadE34

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 711;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6

|||||

Db 139 SGTVGR 144

RESULT 7

S47866
 SPT21 protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YH8010.09; protein YMR179w
 C:Species: Saccharomyces cerevisiae
 C>Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 21-Jul-2000
 C:Accession: S47866; S55126
 R:Natsoulis, G.; Winston, F.; Boeke, J.D.
 Genetics 136, 93-105, 1994
 A:Title: The SPT10 and SPT21 genes of Saccharomyces cerevisiae.
 A:Reference number: S47865; MUID:94186069; PMID:8138180
 A:Accession: S47866
 A:Molecule type: DNA
 A:Residues: 1-758 <NAT>
 A:Cross-references: EMBL:L24436; NID:g402737; PIDN:AAA35078.1; PID:g402738
 R:Churcher, C.M.
 Submitted to the EMBL Data Library, June 1995
 A:Reference number: S55118
 A:Accession: S55126
 A:Molecule type: DNA
 A:Residues: 1-758 <CHD>
 A:Cross-references: EMBL:249808; NID:g854440; PID:g854449; MIPS:YMR179w
 A:Experimental source: strain AB972
 C:Genetics:
 A:Gene: SGD:SPT21
 A:Cross-references: SGD:S0004791; MIPS:YMR179w
 A:Map position: 13R

Query Match 100.0%; Score 30; DB 2; Length 758;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6

|||||
 Db 255 SGTVGR 260

RESULT 8

S77659
 DNA-directed DNA polymerase (EC 2.7.7.7) - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C>Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 23-Mar-2001
 C:Accession: S77659; S72949; S49522
 R:Fsihi, H.; Cole, S.T.
 Mol. Microbiol. 16, 909-919, 1995
 A:Title: The Mycobacterium leprae genome: systematic sequence analysis identifies key ca
 A:Reference number: S77652; MUID:96059637; PMID:7476188
 A:Accession: S77659
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-911 <FSI>
 A:Cross-references: EMBL:246257; NID:g559905; PIDN:CAA86364.1; PID:g559913
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
 R:Smith, D.R.; Robison, K.
 submitted to the EMBL Data Library, November 1993
 A:Description: Mycobacterium leprae cosmid L247.
 A:Reference number: S72589
 A:Accession: S72949
 A:Molecule type: DNA
 A:Residues: 5-911 <SMI>
 A:Cross-references: EMBL:000021; NID:g467141; PIDN:AAA50927.1; PID:g467163
 C:Genetics:
 A:Gene: polA
 A:Start codon: GTG
 C:Superfamily: DNA-directed DNA polymerase I
 C:Keywords: DNA binding; nucleotidyltransferase

Query Match 100.0%; Score 30; DB 2; Length 911;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6

Db 326 SGTVGR 331
 |||||

RESULT 9

JN0901
 endopeptidase Clp ATP-binding chain C - Arabidopsis thaliana
 N:Alternate names: ATP-dependent Clp proteinase regulatory chain; ERD1 protein
 N:Contains: adenosinetriphosphatase (EC 3.6.1.3)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 19-Jan-2001
 C:Accession: JN0901
 R:Kiyosue, T.; Yamaguchi-Shinozaki, K.; Shinozaki, K.
 Biochem. Biophys. Res. Commun. 196, 1214-1220, 1993
 A:Title: Characterization of cDNA for a dehydration-inducible gene that encodes a Clp
 A:Reference number: JN0901; MUID:94071876; PMID:7504470
 A:Accession: JN0901
 A:Molecule type: mRNA
 A:Residues: 1-945 <KIY>
 A:Cross-references: GB:D17582; NID:g443696; PIDN:BAA04506.1; PID:g497629
 A:Note: this protein is homologous to the ATP-binding subunit of ATP-dependent Clp pr
 C:Comment: This protein contains a putative chloroplast targeting signal at the amin
 C:Comment: This protein interacts with a Clp-like protein and functions in the degrad
 C:Genetics:
 A:Gene: ERD1
 C:Function:
 A:Description: allows clpp to hydrolyze polypeptides and proteins, probably by a cha
 e activity; ATP hydrolysis is required for Clp ATP-binding chain
 C:Superfamily: endopeptidase Clp ATP-binding chain
 C:Keywords: ATP; GTP binding; hydrolase; molecular chaperone; nucleotide binding; P-1
 F:316-323/Region: nucleotide-binding motif A (P-loop)
 F:383-388/Region: nucleotide-binding motif B
 F:664-671/Region: nucleotide-binding motif A (P-loop)
 F:732-737/Region: nucleotide-binding motif B
 F:322/Binding site: ATP (Lys) #status predicted
 F:670/Binding site: ATP (Lys) #status predicted

Query Match 100.0%; Score 30; DB 2; Length 945;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6

|||||
 Db 395 SGTVGR 400

RESULT 10

E42400
 ABC-type transport system ATP-binding protein msmk [validated] - Streptococcus mutans
 C:Species: Streptococcus mutans
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 19-Jul-2002
 C:Accession: E42400; C27626
 R:Russell, R.R.; Aduse-Opoku, J.; Sutcliffe, I.C.; Tao, L.; Ferretti, J.J.
 J. Biol. Chem. 267, 4631-4637, 1992
 A:Title: A binding protein-dependent transport system in Streptococcus mutans respons
 A:Reference number: A42400; MUID:92165821; PMID:1537846
 A:Accession: E42400
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-377 <RUS>
 A:Cross-references: GB:M77351; GB:M19349; GB:M30944; GB:M60777; GB:M77352; GB:M77353;
 A:Note: sequence extracted from NCBI backbone (NCBI:83898, NCBIP:83892)
 R:Perretti, J.J.; Huang, T.T.; Russell, R.R.B.
 Infect. Immun. 56, 1585-1588, 1988
 A:Title: Sequence analysis of the glucosyltransferase A gene (gtfa) from Streptococ
 A:Reference number: A27626; MUID:88226936; PMID:2967248
 A:Accession: C27626
 A:Molecule type: DNA
 A:Residues: 1-33 <FER>
 A:Cross-references: EMBL:M19349
 A:Experimental source: strain Ingbritt, serotype C
 C:Genetics:
 A:Gene: msmk

C:Function:

A:Description: involved in the uptake of melibiose, raffinose, and isomaltotriose [valid]
C:Superfamily: inner membrane protein malk; ATP-binding cassette homology
C:Keywords: ATP; nucleotide binding; p-loop
F:21-212/Domain: ATP-binding cassette homology <ABC>
F:38-45/Region: nucleotide-binding motif A (p-loop)

Query Match 96.7%; Score 29; DB 2; Length 377;

Best Local Similarity 83.3%; Pred. No. 88;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6

|||:||

Db 218 SGTIGR 223

RESULT 11

E64055

hypothetical protein HI0216 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999

C:Accession: E64055

F:Leischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.

D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: E64055

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-385 <TIGR>

A:Cross-references: GB:I42023; NID:g1573170; PIDN:AAC21883.1; PID:g1573175; T

C:Superfamily: restriction modification system S chain

Query Match

96.7%; Score 29; DB 2; Length 385;

Best Local Similarity 83.3%; Pred. No. 89;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6

|||:||

Db 268 SGTIGR 273

RESULT 12

H69113

glycine-tRNA ligase (EC 6.1.1.14) - Methanobacterium thermoautotrophicum (strain Delta H

N:Alternate names: glycyl-tRNA synthetase

C:Species: Methanobacterium thermoautotrophicum

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Jun-2002

Accession: H69113

Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.

Ai, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: H69113

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-565 <MTH>

A:Cross-references: GB:AF000937; GB:AF000666; NID:G2622974; PIDN:AAB86312.1; PID:g262298

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH1846

A:Start codon: GTG

C:Superfamily: glycine-tRNA ligase

C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match

96.7%; Score 29; DB 2; Length 565;

Best Local Similarity 83.3%; Pred. No. 1.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6

|||:||

Db 507 SGTIGR 512

RESULT 13

G02500

probable transport protein ALD - human

N:Alternate names: adrenoleukodystrophy protein

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 02-Feb-2001

C:Accession: G02500; S30059

R:Platzter, M.; Bauer, D.; Drescher, B.

submitted to the EMBL Data Library, March 1996

A:Reference number: H01367

A:Accession: G02500

A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-745 <PLA>

A:Cross-references: EMBL:U52111; NID:g1302649; PIDN:AAC51741.1; PID:g1302652

R:Mosser, J.; Douar, A.M.; Sarde, C.O.; Kioschis, P.; Feil, R.; Moser, H.; Poustka, A

Nature 361, 726-730, 1993

A:Title: Putative X-linked adrenoleukodystrophy gene shares unexpected homology with

A:Reference number: S30059; MUID:93180910; PMID:8441467

A:Accession: S30059

A:Molecule type: mRNA

A:Residues: 1-122, 'A', 124-745 <MOS>

A:Cross-references: EMBL:221876; NID:g38590; PIDN:CAA79922.1; PID:g38591

C:Genetics:

A:Gene: GDB:ALD; AMN

A:Cross-references: GDB:118991; OMIM:300100

A:Map position: Xq28-Xq28

A:Introns: 300/3; 361/1; 408/3; 465/1; 496/3; 545/2; 594/1; 622/2; 664/2

C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

C:Keywords: adrenoleukodystrophy; ATP; membrane protein; nucleotide binding; p-loop

F:450-675/Domain: ATP-binding cassette homology <ABC>

F:507-514/Region: nucleotide-binding motif A (p-loop)

F:513/Binding site: ATP (Lys) #status predicted

Query Match

96.7%; Score 29; DB 2; Length 745;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTVGR 6

|||:||

Db 447 SGTIGR 452

RESULT 14

T16843

hypothetical protein T10F2.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-Jan-2000

C:Accession: T16843

R:Miller, N.

submitted to the EMBL Data Library, March 1995

A:Description: The sequence of C. elegans cosmid T10F2.

A:Reference number: Z18589

A:Accession: T16843

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-746 <MIL>

A:Cross-references: EMBL:U23412; NID:g727446; PID:g727447; PIDN:AAA64291.1; CESP:T10F

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:T10F2.1

A:Introns: 32/3; 76/3; 241/3; 412/3; 552/2; 661/3

C:Superfamily: human glycine-tRNA ligase; amino acid-tRNA ligase repeat homology

Query Match

96.7%; Score 29; DB 2; Length 746;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
|||:|
Db 665 SGTIGR 670

RESULT 15
I52333
G1 phase-specific gene - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C:Accession: I52333
R:Wu, G.; Su, S.; Kung, T.Y.; Bird, R.C.
Biochem. Cell Biol. 71, 372-380, 1993
A:Title: Molecular cloning of G1 phase mRNAs from a subtractive G1 phase cDNA library.
A:Reference number: I52333; MUID:94168720; PMID:8123253
A:Accession: I52333
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-109 <RES>
A:Cross-references: GB:S70622; NID:9545857; PIDN:AAB30172.1; PID:9545858
A:Experimental source: HeLa S3 cells

Query Match 90.0%; Score 27; DB 2; Length 109;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTVGR 6
|||:|
Db 75 AGTVGR 80

Search completed: February 26, 2003, 08:40:23
Job time : 7.53846 secs

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13

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